

GenCore version 5.1.7

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OM nucleic - nucleic search, using sw model

Run on: March 4, 2006, 01:46:27 ; Search time 2853.47 Seconds
(without alignments)
295.138 Million cell updates/sec

Title: US-09-701-583A-9

Perfect score: 18

Sequence: 1 cggatgctctatttga 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 106998

Minimum DB seq length: 0

Maximum DB seq length: 4033

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_hc:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_ges1:*

10: gb_ges2:*

11: gb_ges3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12.4	68.9	24	9	AZ846667 2M0146P24
2	12.4	68.9	34	1	AU258674 AU258674
3	12.4	68.9	37	9	BZ287861 SALK_0212
4	12.4	68.9	40	9	AZ822722 2M0096008
5	11.8	65.6	20	10	CL313440 mth2-128N
6	11.8	65.6	30	10	CZ469644 c04964-5p
7	11.8	65.6	37	10	CZ477101 d10098-3p
8	11.6	64.4	29	10	AB081925 Drosophila
9	11.6	64.4	30	10	CZ487985 f05420-3p
10	11.4	63.3	21	9	AZ402083 1M0169A15
11	11.4	63.3	28	9	AZ471813 1M0286D06
12	11.4	63.3	31	10	AG192945 Pan trogl
13	11.4	63.3	36	6	CA851372 D13A08_A0
14	11.2	62.2	24	10	AJ587601 Arabidops
15	11.2	62.2	27	9	BZ768666 SALK_1405
16	11.2	62.2	28	1	AI690628 tx98g09.x
17	11.2	62.2	30	10	CZ470021 c05477b-5
18	11.2	62.2	34	1	AV852639 AV852639
19	11	61.1	37	10	CZ489987 f07187-5p
20	11	61.1	39	1	AU006827 AU006827
21	10.8	60.0	27	9	AZ478637 1M0298B23
22	10.8	60.0	29	9	AZ803680 2M0064009

23	10.8	60.0	31	1	AU009970
24	10.8	60.0	31	1	AU009989
25	10.8	60.0	31	10	BX532321 Arabidops
26	10.8	60.0	31	10	BX532876 Arabidops
c 27	10.8	60.0	32	6	CA851642 D16A01_B1
c 28	10.8	60.0	33	1	AV836794
29	10.8	60.0	33	8	D11586
30	10.8	60.0	34	8	D11855
31	10.8	60.0	34	8	N30120
32	10.8	60.0	34	10	BX661869 Arabidops
33	10.8	60.0	36	9	AZ398982 1M0164D08
34	10.8	60.0	36	9	AZ398982 1M0566E15
c 35	10.8	60.0	36	10	CZ551808
36	10.8	60.0	36	10	CZ919151 4021012A0
c 37	10.8	60.0	36	10	AL944589 Arabidops
c 38	10.8	60.0	37	1	AI016852
39	10.8	60.0	37	10	AL944588 Arabidops
40	10.8	60.0	38	10	CZ559623 PL000353-5
41	10.8	60.0	40	10	BX536158 Arabidops
c 42	10.6	58.9	24	9	AZ763574
c 43	10.6	58.9	25	9	AZ768828 1M0559P01
44	10.6	58.9	25	10	CZ467409 c01749-3p
c 45	10.6	58.9	25	10	CZ483624 f01137-3p

ALIGNMENTS

RESULT 1

AZ846667

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

AZ846667 24 bp DNA linear GSS 21-FEB-2001
2M0146P24R Mouse 10kb plasmid UGCLM library Mus musculus genomic
clone UGCLM0146P24 R, genomic survey sequence.

AZ846667

AZ846667.1 GI:13027929

GSS.

Mus musculus (house mouse)

Mus musculus

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 24)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Rielly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert length: 10000 Std Error: 0.00

Plate: 0146 row: P column: 24

Seq primer: CACACGAAACACCTAIGACC

Class: plasmid ends

High quality sequence stop: 24.

Location/Qualifiers

1..24

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0146P24"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UGCLM library"

/note="Vector: PWD42nv; Purified genomic DNA from M."

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: gdunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0096 row: 0 column: 08
 Seq primer: CGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 40.

FEATURES

source
 1. .40
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M096008"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCCIM library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (Gill4732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 68.9%; Score 12.4; DB 9; Length 40;
 Best Local Similarity 92.9%; Pred. No. 1.8e+05;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CATGCTCTATTGTTGT 17
 |||||
 Db 5 CATGCTCTACTTGT 18

RESULT 5

CL313440/c
 LOCUS
 DEFINITION
 mch2-128N01 OP Medicago truncatula BAC end sequences Medicago truncatula genomic 5', genomic survey sequence.

CL313440
 CL313440.1 GI:44831114
 GSS.

Medicago truncatula (barrel medic)
 SOURCE
 Medicago truncatula

ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliales; Medicago.

REFERENCE 1 (bases 1 to 20)

AUTHORS
 TITLE
 JOURNAL
 COMMENT

Jakab, J., Deak, G., Kevei, Z., Karchesz, K., Sarai, E., Kiss, P., Kereszt, A., Kaló, P., Endre, G., and Kiss, G.B.
 Medicago truncatula BAC end sequencing
 Unpublished (2004)
 Contact: Deak, G.
 Alfalfa Genomics Group; Medicago Genetics Group
 Agricultural Biotechnology Center; Biological Research Center
 P.O. Box 411, Hungary, H-2100 Godollo, Szent-Györgyi Albert ut 4.;
 P.O. Box 531, Hungary, H-6701 Szeged, Temesvári krt. 62
 Tel: 3628526142
 Fax: 3628526193
 Email: gdeak@abc.hu
 Plate: 128 row: N column: 01
 Seq primer: OP Reverse
 Class: BAC ends.

FEATURES

source
 1. .20
 Location/Qualifiers
 /organism="Medicago truncatula"
 /mol_type="genomic DNA"
 /cultivar="Jemalong"
 /isolate="A17"
 /db_xref="taxon:3880"
 /sex="Hermaphrodite"
 /clone_lib="Medicago truncatula BAC end sequences"
 /note="Organ: Leaf; Vector: pBeloll; Site: HindIII;
 Site 2: HindIII; Construction of a bacterial artificial chromosome library of Medicago truncatula and identification of clones containing ethylene-response genes. Theor Appl Genet (1999) 98: 638-646 Y.-W. Nam; R.V. Pennetsa; G. Endre; P. Uribe; D. Kim; D.R. Cook"

ORIGIN

Query Match 65.6%; Score 11.8; DB 10; Length 20;
 Best Local Similarity 81.2%; Pred. No. 3.6e+05;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGCATGCTCTATTGTTG 16
 |||||
 Db 16 CGGCATTNTTTTGTG 1

RESULT 6

LOCUS
 DEFINITION
 CZ469644 30 bp DNA linear GSS 29-APR-2005
 c04964-Sprime Exelixis piggyBac PB insertions Drosophila melanogaster genomic Sequence recovered from 5' end of piggyBac, genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

CZ469644
 CZ469644.1 GI:62963657
 GSS.
 Drosophila melanogaster (fruit fly)

ORGANISM
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 30)

AUTHORS

Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A., Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.L., Ryner, L., Cheung, L.M., Chong, A., Erickson, C., Fisher, W.W., Greer, K., Harcourt, S.R., Howie, E., Jakkula, L., Joo, D., Killpack, K., Lauer, A., Mazotta, J., Smith, R.D., Stevens, L.M., Stuber, C., Tan, L.R., Ventura, R., Woo, A., Zakrajsek, I., Zhao, L., Chen, F., Swimmer, C., Kopczyński, C., Duyk, G., Winberg, M.L. and Margolis, J.
 A complementary transposon tool kit for Drosophila melanogaster using P and piggyBac
 Nat. Genet. 36 (3), 283-287 (2004)

TITLE

JOURNAL
 PUBLISHED
 COMMENT
 Contact: Roger A Hoskins
 Berkeley Drosophila Genome Project
 Lawrence Berkeley National Laboratory
 Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
 Tel: 510 486 4015
 Fax: 510 486 6798

Email: RHoskins@lbl.gov
 Sequence recovery method was inverse PCR.
 Sequence orientation is forward strand relative to 5' end of piggyBac element.
 The piggyBac insertion position is 27 in the 30 bases. This insertion position refers to the first base of the 4 base TTA target recognition sequence.
 Class: transposon insertion site.
 Location/Qualifiers
 1..30
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /strain="isogenic w- strain"
 /db_xref="taxon:7227"
 /clone_lib="Exelixis piggyBac PB insertions"
 /note="Vector: piggyBac PB (GenBank accession number AY15146); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. We remobilized the PB element using Hsp70:piggyBac transposase from a single ammunition element on either the X or third chromosome. We induced transposase expression by immersing bottles in a circulating 37°C water bath for a daily (days 3-10 after egg-laying) 1-h heat shock. We outcrossed the resulting dysgenic males to an isogenic w- strain. New insertions were identified on the basis of a change in eye color (third chromosome ammunition) or the appearance of w+ male progeny (X chromosome ammunition). All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic sequence by inverse PCR."

FEATURES

source

1..30
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /strain="isogenic w- strain"
 /db_xref="taxon:7227"
 /clone_lib="Exelixis piggyBac PB insertions"
 /note="Vector: piggyBac PB (GenBank accession number AY15146); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. We remobilized the PB element using Hsp70:piggyBac transposase from a single ammunition element on either the X or third chromosome. We induced transposase expression by immersing bottles in a circulating 37°C water bath for a daily (days 3-10 after egg-laying) 1-h heat shock. We outcrossed the resulting dysgenic males to an isogenic w- strain. New insertions were identified on the basis of a change in eye color (third chromosome ammunition) or the appearance of w+ male progeny (X chromosome ammunition). All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic sequence by inverse PCR."

ORIGIN

Query Match 65.6%; Score 11.8; DB 10; Length 30;
 Best Local Similarity 86.7%; Pred. No. 3.6e+05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GCATGCTCTATTTTGT 17

Db 12 GCATGCTCTATTTT 26

RESULT 7

Cz477101/c
 LOCUS
 DEFINITION
 d10098-3prime Exelixis P element XP insertions Drosophila melanogaster genomic Sequence recovered from 3' end of P element, genomic survey sequence.

Cz477101

Cz477101.1 GI:62972138

GSS.

Drosophila melanogaster (fruit fly)

ORGANISM

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 37)

REFERENCE

AUTHORS

Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A., Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L., Ryner,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W., Greer,K., Hartouni,S.R., Howie,E., Jakkula,L., Joo,D., Killpack,K., Laufer,A., Mazzotta,J., Smith,R.D., Stevens,L.M., Stuber,C., Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F., Swimmer,C., Kopyzynski,C., Duyk,G., Winberg,M.L. and Margolis,J.
 A complementary transposon tool kit for Drosophila melanogaster using P and piggyBac
 Nat. Genet. 36 (3), 283-287 (2004)

14981521

PUBMED

COMMENT

Contact: Roger A Hoskins
 Berkeley Drosophila Genome Project
 Lawrence Berkeley National Laboratory
 Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
 Tel: 510 486 4015

Fax: 510 486 6798
 Email: RHoskins@lbl.gov
 Sequence recovery method was inverse PCR.
 Sequence orientation is forward strand relative to 5' end of P element.
 The P element insertion position is 1 in the 37 bases. This insertion position refers to the first base of the 8 base target recognition sequence.
 Class: transposon insertion site.
 Location/Qualifiers
 1..37
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /strain="isogenic w- strain"
 /db_xref="taxon:7227"
 /clone_lib="Exelixis P element XP insertions"
 /note="Vector: P element XP (GenBank accession number AY15149); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. For the P element XP, we selected an easily mobilized ammunition element among inserts hopped onto the Binsyncy balancer. New insertions were collected in vials from dysgenic females using the standard chromosomal source of transposase, delta2-3. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability and used for recovery of flanking genomic sequence by inverse PCR."

FEATURES

source

1..37
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /strain="isogenic w- strain"
 /db_xref="taxon:7227"
 /clone_lib="Exelixis P element XP insertions"
 /note="Vector: P element XP (GenBank accession number AY15149); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. For the P element XP, we selected an easily mobilized ammunition element among inserts hopped onto the Binsyncy balancer. New insertions were collected in vials from dysgenic females using the standard chromosomal source of transposase, delta2-3. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability and used for recovery of flanking genomic sequence by inverse PCR."

ORIGIN

Query Match 65.6%; Score 11.8; DB 10; Length 37;
 Best Local Similarity 86.7%; Pred. No. 3.6e+05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGCATGCTCTATTTT 15

Db 29 CTGCATGCTCTCTTTT 15

RESULT 8

AB081925/c

LOCUS

DEFINITION

AB081925 Drosophila melanogaster DNA, clone:1(2)SH2 0218, genomic survey sequence.

AB081925

AB081925.1 GI:21623935

GSS.

Drosophila melanogaster (fruit fly)

ORGANISM

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

AUTHORS

Oh,S.W., Kingsley,T., Shin,H.H., Zheng,Z., Chen,H.W., Chen,X., Wang,H., Ruan,P., Moody,M. and Hou,S.X.
 A p-element insertion screen identified mutations in 455 novel essential genes in Drosophila

Genetics 163 (1), 195-201 (2003)

12586707

2 (bases 1 to 29)

REFERENCE

AUTHORS

Oh,S., Kingsley,T., Shin,H., Zheng,Z., Chen,H. and Hou,S.

Direct Submission

Submitted (21-MAR-2002) Suwan Oh, The Laboratory of Immunobiology,

National Institutes of Health, National Cancer Institute, USA

Frederick, 1050 Boyles St., Frederick, Maryland 21702-1201, USA

(E-mail:ohsuwan@mail.ncifcrf.gov, Tel:1-301-846-7314,

Fax:1-301-846-6145)

1..29

Location/Qualifiers

/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/db_xref="taxon:7227"

/clone="1(2)SH2 0218"

ORIGIN

Query Match 64.4%; Score 11.6; DB 10; Length 29;
 Best Local Similarity 77.8%; Pred. No. 4.5e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGGCATGCTCTATTGTGA 18
 |||||
 DB 29 CAGCAGGCTCAATTGTGA 12

RESULT 9
 C2487985/c
 LOCUS
 DEFINITION f05420-3prime Exelixis piggyBac WH insertions Drosophila melanogaster genomic Sequence recovered from 3' end of piggyBac, genomic survey sequence.

ACCESSION C2487985
 VERSION C2487985.1 GI:62985423
 KEYWORDS GSS.
 ORGANISM Drosophila melanogaster (fruit fly)
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 30)
 AUTHORS Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A., Singh,C.M., Buchholz,R., Demeky,M., Fawcett,R., Francis-Lang,H.L., Ryner,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W., Greer,K., Hartouni,S.R., Howie,E., Jakkula,L., Joo,D., Killpack,K., Laufer,A., Mazzotta,J., Smith,R.D., Stevens,L.M., Stuber,C., Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F., Swimmer,C., Koczynski,C., Duyk,G., Winberg,M.L. and Margolis,J.
 TITLE A complementary transposon tool kit for Drosophila melanogaster using P and piggyBac

JOURNAL Nat. Genet. 36 (3), 283-287 (2004)
 PUBMED 14981521
 COMMENT Contact: Roger A Hoskins
 Berkeley Drosophila Genome Project
 Lawrence Berkeley National Laboratory
 Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
 Tel: 510 486 4015
 Fax: 510 486 6798
 Email: Rhoskins@lbl.gov

Sequence recovery method was inverse PCR.
 Sequence orientation is forward strand relative to 5' end of piggyBac element.
 The piggyBac insertion position is 1 in the 30 bases. This insertion position refers to the first base of the 4 base TTAA target recognition sequence.
 Class: transposon insertion site.

FEATURES
 source
 1..30
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /strain="isogenic w- strain"
 /db_xref="taxon:7227"
 /clone_lib="Exelixis piggyBac WH insertions"
 /note="Vector: piggyBac WH (GenBank accession number AY151148); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. We remobilized the WH element using the constitutive alpha-1 tubulin:piggyBac transposase source. We remobilized the WH element from a single ammunition element on the Binsincy balancer chromosome in dysgenic females. We outcrossed dysgenic virgin females in vials to the isogenic w- strain and selected new hops in the following generation. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic sequence by inverse PCR."

ORIGIN

Query Match 64.4%; Score 11.6; DB 10; Length 30;

Best Local Similarity 77.8%; Pred. No. 4.5e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGGCATGCTCTATTGTGA 18
 |||||
 DB 19 CGGCTTTCTTTTTTTA 2

RESULT 10

AZ402083

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0169 row: A column: 15

Seq primer: CGTTGTAACAGCGGCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1..21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUCIM0169A15"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUCIM library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 63.3%; Score 11.4; DB 9; Length 21;
 Best Local Similarity 92.3%; Pred. No. 5.7e+05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GCATGCTATTTT 15
 |||||
 Db 4 GCATTTCTATTTT 16

RESULT 11
 AZ471813/c
 LOCUS
 DEFINITION IM0286D06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0286D06 R, genomic survey sequence.

ACCESSION AZ471813
 VERSION
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 28)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Ielam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0286 row: D column: 06
 Seq primer: CACACAGGAACACGTATGACC
 Class: plasmid ends
 High quality sequence stop: 28.

FEATURES
 source
 1..28
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0286D06"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 63.3%; Score 11.4; DB 9; Length 28;
 Best Local Similarity 92.3%; Pred. No. 5.7e+05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CATGCTATTTTG 16
 |||||
 Db 14 CATGGCTATTTTG 2

RESULT 12
 AG192945
 LOCUS
 DEFINITION Pan troglodytes DNA, clone: RP43-069M06.T7, genomic survey sequence.

ACCESSION AG192945
 VERSION
 KEYWORDS
 SOURCE GSS.
 ORGANISM Pan troglodytes (chimpanzee)
 Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Pan.

REFERENCE 1
 AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Run, C. J., Hoon, S. T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
 TITLE BAC end sequences of Library RP-43
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 31)
 AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Run, C. J., Hoon, S. T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
 TITLE Direct Submission
 JOURNAL Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC); S2, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
 (E-mail: red2stone@mail.krribb.re.kr, URL: http://phs.grc.krribb.re.kr/, Tel: 82-42-866-7181, Fax: 82-42-860-4409)
 COMMENT Clones are derived from the chimpanzee BAC library RP-43. This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

PRIMERS
 Sequencing: T7
 LIBRARY
 Vector : pBACe3.6
 R.Site 1 : EcoRI
 R.Site 2 : EcoRI
 Location/Qualifiers
 1..31
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 /clone="RP43-069M06.T7"
 /sex="male"
 /cell_type="lymphocytes"
 /clone_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN
 Query Match 63.3%; Score 11.4; DB 10; Length 31;
 Best Local Similarity 92.3%; Pred. No. 5.7e+05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 TGTCTATTTGTA 18
 |||||
 Db 17 TGTCTATTTGTA 29

RESULT 13
 CA851372/c
 LOCUS
 DEFINITION D13A08 A08.02.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max cDNA clone D13A08 5', mRNA sequence.

ACCESSION CA851372
 VERSION CA851372.1 GI:33388165

KEYWORDS
SOURCE EST.
ORGANISM Glycine max (soybean)
 Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
REFERENCE 1 (bases 1 to 36)
AUTHORS Alkharouf, N., Khan, R. and Matthews, B.
TITLE Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode
JOURNAL Genome 47 (2), 380-388 (2004)
PUBMED 15060591
COMMENT Contact: Alkharouf, N.W.
 Soybean Genomics and Improvement Laboratory (SGIL)
 US Department of Agriculture (USDA), ARS, PSI
 Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA
 Tel: 301 504 5750
 Fax: 301 504 5728
 Email: alkharouf@ba.ars.usda.gov.
FEATURES
 source
 1..36
 Location/Qualifiers
 /organism="Glycine max"
 /mol_type="mRNA"
 /cultivar="Peking"
 /db_xref="taxon:3847"
 /clone="D13A08"
 /tissue_type="Roots"
 /dev_stage="Seedlings"
 /clone_lib="cDNA Peking library 2, 4 day SCN3"
 /note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from Peking roots 2 and 4 days past invasion."
ORIGIN
 Query Match 63.3%; Score 11.4; DB 6; Length 36;
 Best Local Similarity 80.0%; Pred. No. 5.8e+05;
 Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 4 CATGCTATTTTGTA 18
 || |||||
 Db 15 CANNCTATTTTTAA 1
RESULT 14
AJ587601
LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone 298H08, genomic survey sequence.
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 298H08, genomic survey sequence.
ACCESSION AJ587601
VERSION AJ587601.1 GI:37937225
KEYWORDS GSS; left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1
AUTHORS Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechold, N., Cruaud, C., Derose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED 12446565
REFERENCE 2 (bases 1 to 24)
AUTHORS Balzerque, S.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border

to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).
FEATURES
 Location/Qualifiers
 1..24
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /db_xref="taxon:3702"
 /clone="298H08"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Wassilewskija"
 /note="T-DNA flanking sequence left border"
 misc_feature
 1..24
 /note="T-DNA flanking sequence left border"
ORIGIN
 Query Match 62.2%; Score 11.2; DB 10; Length 24;
 Best Local Similarity 81.2%; Pred. No. 7.2e+05;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 GGCATGCTATTTTGT 17
 ||| ||| ||| ||| |||
 Db 1 GGCCTGTGTAATTGT 16
RESULT 15
BZ768666/c
LOCUS Arabidopsis thaliana T-DNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_140548.46.70.x, genomic survey sequence.
ACCESSION BZ768666
VERSION BZ768666.1 GI:28942307
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 27)
AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salg.edu
 This is single pass sequence recovered from the left border of T-DNA.
FEATURES
 Location/Qualifiers
 1..27
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone="SALK_140548.46.70.x"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more T-DNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 62.2%; Score 11.2; DB 9; Length 27;
Best Local Similarity 81.2%; Pred. No. 7.2e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCATGCTCTATTTTGTGTA 18
||| ||| ||| ||| ||| ||| ||| |||
Db 26 GCTTGCTCTCTTTTATA 11

Search completed: March 4, 2006, 03:39:01
Job time : 2857.47 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 4, 2006, 01:49:48 ; Search time 375.632 Seconds
(without alignments)
396.263 Million cell updates/sec

Title: US-09-701-583A-9
Perfect score: 18
Sequence: 1 cggcatgtctatttga 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 10900902

Minimum DB seq length: 0

MaximumDB:seqlength=406

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	5	US-10-146-058-72 Sequence 72, Appl
2	18	100.0	18	6	US-10-220-033-4 Sequence 4, Appl
3	18	100.0	18	9	US-10-984-919-1209 Sequence 1209, Ap
4	16	88.9	16	9	US-10-984-919-1277 Sequence 40, Appl
5	16	88.9	20	6	US-10-189-267-40 Sequence 185, App
6	16	88.9	20	6	US-10-189-267-185 Sequence 529, App
7	16	88.9	20	9	US-10-984-919-529 Sequence 116, App
8	14.8	82.2	20	6	US-10-189-267-116 Sequence 243, App
9	14.8	82.2	20	6	US-10-189-267-243 Sequence 243, App
10	14.8	82.2	25	5	US-10-098-263B-91037 Sequence 91037, A
11	14.8	82.2	25	10	US-11-036-317-121656 Sequence 121656,
12	14.8	82.2	25	10	US-11-060-756-190386 Sequence 190386,
13	14.8	82.2	25	10	US-11-060-756-259860 Sequence 259860,
14	14.4	80.0	25	8	US-10-719-900-865692 Sequence 865692,
15	14.4	80.0	25	10	US-11-036-317-194446 Sequence 194446,
16	14.4	80.0	25	10	US-11-036-317-253543 Sequence 253543,
17	14.4	80.0	25	10	US-11-036-317-276997 Sequence 276997,
18	14.4	80.0	25	10	US-11-036-317-310713 Sequence 310713,
19	14.4	80.0	25	10	US-11-036-317-334637 Sequence 334637,
20	14.4	80.0	25	10	US-11-036-317-383155 Sequence 383155,
21	14	77.8	20	6	US-10-189-267-54 Sequence 197, Appl
22	14	77.8	20	6	US-10-189-267-197 Sequence 197, Appl
23	14	77.8	25	10	US-11-036-317-474175 Sequence 474175,

Sequence 777184,
Sequence 180828,
Sequence 583979,
Sequence 715769,
Sequence 198172,
Sequence 229607,
Sequence 239950,
Sequence 294363,
Sequence 322759,
Sequence 439359,
Sequence 7, Appli
Sequence 55957, A
Sequence 518120,
Sequence 60048, A
Sequence 589217,
Sequence 592572,
Sequence 808618,
Sequence 51384, A
Sequence 51387, A
Sequence 51389, A
Sequence 51390, A
Sequence 271471,
Sequence 777184,
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Sequence 583979,
Sequence 715769,
Sequence 198172,
Sequence 229607,
Sequence 239950,
Sequence 294363,
Sequence 322759,
Sequence 439359,
Sequence 7, Appli
Sequence 55957, A
Sequence 518120,
Sequence 60048, A
Sequence 589217,
Sequence 592572,
Sequence 808618,
Sequence 51384, A
Sequence 51387, A
Sequence 51389, A
Sequence 51390, A
Sequence 271471,

ALIGNMENTS

RESULT 1

US-10-146-058-72
; Sequence 72, Application US/10146058
; Publication No. US20030040499A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS: 137
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,058
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/535,249
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William B.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 72:

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/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ MOLECULE TYPE: DNA (genomic)
/ ANTI-SENSE: YES
US-10-146-058-72

Query Match      100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCATGCTCTATTGTGTA 18
Db 1 CGGCATGCTCTATTGTGTA 18

RESULT 2
US-10-220-033-4
/ Sequence 4, Application US/10220033
/ Publication No. US20030186906A1
/ GENERAL INFORMATION:
/ APPLICANT: Schlingensiepen, Karl-Hermann
/ TITLE OF INVENTION: Mixture comprising an inhibitor or suppressor of a gene
/ TITLE OF INVENTION: and a molecule binding to an expression product of that
/ TITLE OF INVENTION: gene
/ FILE REFERENCE: P68119USO
/ CURRENT APPLICATION NUMBER: US/10/220.033
/ CURRENT FILING DATE: 2003-03-17
/ PRIOR APPLICATION NUMBER: PCT/EP01/02694
/ PRIOR FILING DATE: 2001-03-10
/ PRIOR APPLICATION NUMBER: EP00105190.3
/ PRIOR FILING DATE: 2000-03-11
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 18
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: antisense
/ OTHER INFORMATION: oligonucleotide
US-10-220-033-4

Query Match      100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCATGCTCTATTGTGTA 18
Db 1 CGGCATGCTCTATTGTGTA 18

RESULT 3
US-10-984-919-1209
/ Sequence 1209, Application US/10984919
/ Publication No. US20050130927A1
/ GENERAL INFORMATION:
/ APPLICANT: Schlingensiepen, Karl-Hermann
/ TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
/ FILE REFERENCE: 10496/P63763USO
/ CURRENT APPLICATION NUMBER: US/10/984.919
/ CURRENT FILING DATE: 2004-11-10
/ PRIOR APPLICATION NUMBER: US/09/341.700
/ PRIOR FILING DATE: 1999-09-24
/ PRIOR APPLICATION NUMBER: PCT/EP98/00497
/ PRIOR FILING DATE: 1998-01-30
/ PRIOR APPLICATION NUMBER: EP 97 101 531.8
/ PRIOR FILING DATE: 1997-01-31
/ NUMBER OF SEQ ID NOS: 1764
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 18
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: antisense oligonucleotide
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/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1209
/ LENGTH: 18
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:
/ OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-1209

Query Match      100.0%; Score 18; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCATGCTCTATTGTGTA 18
Db 1 CGGCATGCTCTATTGTGTA 18

RESULT 4
US-10-984-919-1277
/ Sequence 1277, Application US/10984919
/ Publication No. US20050130927A1
/ GENERAL INFORMATION:
/ APPLICANT: Schlingensiepen, Karl-Hermann
/ TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
/ FILE REFERENCE: 10496/P63763USO
/ CURRENT APPLICATION NUMBER: US/10/984.919
/ CURRENT FILING DATE: 2004-11-10
/ PRIOR APPLICATION NUMBER: US/09/341.700
/ PRIOR FILING DATE: 1999-09-24
/ PRIOR APPLICATION NUMBER: PCT/EP98/00497
/ PRIOR FILING DATE: 1998-01-30
/ PRIOR APPLICATION NUMBER: EP 97 101 531.8
/ PRIOR FILING DATE: 1997-01-31
/ NUMBER OF SEQ ID NOS: 1764
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1277
/ LENGTH: 16
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:
/ OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-1277

Query Match      88.9%; Score 16; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCATGCTCTATTGTG 16
Db 1 CGGCATGCTCTATTGTG 16

RESULT 5
US-10-189-267-40
/ Sequence 40, Application US/10189267
/ Publication No. US20040006030A1
/ GENERAL INFORMATION:
/ APPLICANT: Brett P. Monia
/ APPLICANT: Susan M. Freier
/ APPLICANT: Kenneth W. Dobie
/ TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
/ FILE REFERENCE: PTS-0038
/ CURRENT APPLICATION NUMBER: US/10/189.267
/ CURRENT FILING DATE: 2002-07-02
/ NUMBER OF SEQ ID NOS: 284
/ SEQ ID NO 40
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-40

Query Match 88.9%; Score 16; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCATGCTCTATTG 16
Db 5 CGGCATGCTCTATTG 20

RESULT 6
US-10-189-267-185/c
; Sequence 185, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 185
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-189-267-185

Query Match 88.9%; Score 16; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCATGCTCTATTG 16
Db 16 CGGCATGCTCTATTG 1

RESULT 7
US-10-984-919-529
; Sequence 529, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlingsiepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 529
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-529

Query Match 88.9%; Score 16; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GCATGCTATTGTA 18
Db 1 GCATGCTATTGTA 16

RESULT 8
US-10-189-267-116
; Sequence 116, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 116
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-116

Query Match 82.2%; Score 14.8; DB 6; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGGCATGCTCTATTGTA 18
Db 1 CGGCATGCTCGATTGTA 18

RESULT 9
US-10-189-267-243/c
; Sequence 243, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 243
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-243

Query Match 82.2%; Score 14.8; DB 6; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGGCATGCTCTATTGTA 18
Db 20 CGGCATGCTCGATTGTA 3

RESULT 10
US-10-098-263B-91037
; Sequence 91037, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1

FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036.317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 194446
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-194446

Query Match 80.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.5e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCATGCTCTATTTCGTA 18
|||||
Db 25 GCATGCTCTATTTCGTA 10

Search completed: March 4, 2006, 07:04:14
Job time : 375.632 secs

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OM nucleic - nucleic search, using sw model

Run on: March 4, 2006, 01:58:42 ; Search time 446.211 Seconds
(without alignments)
88.444 Million cell updates/sec

Title: US-09-701-583A-9
Perfect score: 18
Sequence: 1 cggcatgctctatttcta 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters: 11581468

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:

- 1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:
- 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
- 3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
- 4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
- 5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
- 6: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
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- 8: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
- 9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
- 10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
- 11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
- 12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	94.4	25	US-11-121-849-319164	Sequence 319164,
2	17	94.4	25	US-11-121-849-319625	Sequence 319625,
3	13.8	76.7	22	US-10-310-914A-461071	Sequence 461071,
4	13.8	76.7	22	US-10-310-914A-378741	Sequence 378741,
5	13.4	74.4	22	US-10-310-914A-1375953	Sequence 1375953,
6	13.4	74.4	25	US-11-121-849-151115	Sequence 151115,
7	13.4	74.4	25	US-11-136-527-153306	Sequence 153306,
8	13.4	74.4	25	US-11-136-527-153312	Sequence 153312,
9	13.4	74.4	25	US-11-136-527-153317	Sequence 153317,
10	13.4	74.4	25	US-11-136-527-153325	Sequence 153325,
11	13.4	74.4	25	US-11-136-527-153326	Sequence 153326,
12	13.4	74.4	25	US-11-136-527-153341	Sequence 153341,
13	13.4	74.4	25	US-11-121-849-245961	Sequence 245961,
14	13.2	73.3	25	US-11-101-244-1437211	Sequence 1437211,
15	13	72.2	19	US-11-101-244-1437212	Sequence 1437212,
16	13	72.2	19	US-11-101-244-1437218	Sequence 1437218,
17	13	72.2	19	US-11-083-784-1437211	Sequence 1437211,
18	13	72.2	19	US-11-083-784-1437212	Sequence 1437212,
19	13	72.2	19	US-11-083-784-1437218	Sequence 1437218,
20	13	72.2	19	US-11-121-849-150728	Sequence 150728,

c	21	13	72.2	23	8	US-10-310-914A-680711	Sequence 680711,
	22	13	72.2	24	8	US-10-310-914A-986600	Sequence 986600,
	23	13	72.2	25	12	US-11-121-849-108655	Sequence 108655,
c	24	12.8	71.1	18	8	US-10-310-914A-291549	Sequence 291549,
c	25	12.8	71.1	19	8	US-10-310-914A-1023769	Sequence 1023769,
	26	12.8	71.1	19	10	US-11-101-244-617220	Sequence 617220,
	27	12.8	71.1	19	10	US-11-101-244-617251	Sequence 617251,
	28	12.8	71.1	19	10	US-11-101-244-1125173	Sequence 1125173,
	29	12.8	71.1	19	11	US-11-083-784-617220	Sequence 617220,
	30	12.8	71.1	19	11	US-11-083-784-617251	Sequence 617251,
	31	12.8	71.1	19	11	US-11-083-784-1125173	Sequence 1125173,
c	32	12.8	71.1	20	8	US-10-310-914A-375180	Sequence 375180,
c	33	12.8	71.1	21	8	US-10-310-914A-289791	Sequence 289791,
c	34	12.8	71.1	22	8	US-10-310-914A-476895	Sequence 476895,
c	35	12.8	71.1	22	8	US-10-310-914A-805261	Sequence 805261,
c	36	12.8	71.1	22	8	US-10-310-914A-805263	Sequence 805263,
c	37	12.8	71.1	23	8	US-10-310-914A-375181	Sequence 375181,
c	38	12.8	71.1	23	8	US-10-310-914A-805246	Sequence 805246,
c	39	12.8	71.1	23	8	US-10-310-914A-1023780	Sequence 1023780,
c	40	12.8	71.1	24	8	US-10-310-914A-553186	Sequence 553186,
	41	12.8	71.1	24	8	US-10-310-914A-1343860	Sequence 1343860,
	42	12.8	71.1	25	8	US-10-310-914A-564999	Sequence 564999,
	43	12.8	71.1	25	12	US-11-121-849-7342	Sequence 7342, Ap
	44	12.8	71.1	25	12	US-11-121-849-112895	Sequence 112895,
	45	12.8	71.1	25	12	US-11-121-849-150728	Sequence 150728,

ALIGNMENTS

RESULT 1

US-11-121-849-319164
; Sequence 319164, Application US/11121849
; Publication No. US2005027080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 319164
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-319164

Query Match 94.4% Score 17; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGCATGCTCTATTGTGA 18
|||||
Db 1 GGCATGCTCTATTGTGA 17

RESULT 2

US-11-121-849-319625
; Sequence 319625, Application US/11121849
; Publication No. US2005027080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03

; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 319625
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-319625

Query Match 94.4%; Score 17; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGCATGCTCTATTGTGA 18
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GGCATGCTCTATTGTGA 17

RESULT 3
US-10-310-914A-461071
; Sequence 461071, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 461071
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-461071

Query Match 76.7%; Score 13.8; DB 8; Length 22;
Best Local Similarity 47.1%; Pred. No. 8.5e+02;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGCATGCTCTATTGTGA 18
| | | | | | | | | | | | | | | | | | | | | |
Db 6 GUCAUGUCUACUUGUA 22

RESULT 4
US-10-310-914A-378741/c
; Sequence 378741, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 378741
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-378741

Query Match 76.7%; Score 13.8; DB 8; Length 24;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGCATGCTCTATTGTGA 18
| | | | | | | | | | | | | | | | | | | | | |
Db 17 GGCATTTGTATTGTGA 1

RESULT 5

US-10-310-914A-1375953/c
; Sequence 1375953, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1375953
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1375953

Query Match 74.4%; Score 13.4; DB 8; Length 22;
Best Local Similarity 93.3%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGCATGCTCTATTGTG 16
| | | | | | | | | | | | | | | | | | | | | |
Db 22 GGCATGCTCTATTGTG 8

RESULT 6

US-11-121-849-151115
; Sequence 151115, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 151115
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-151115

Query Match 74.4%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CATGCTCTATTGTGA 18
| | | | | | | | | | | | | | | | | | | | | |
Db 1 CATGCTCTATTGTGA 15

RESULT 7

US-11-136-527-153306
; Sequence 153306, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136.527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294

;; PRIOR FILING DATE: 2005-05-26
;; NUMBER OF SEQ ID NOS: 362830
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 153306
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: Probe
US-11-136-527-153306

Query Match 74.4%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GCATGCTCTATTGT 17
|||
Db 1 GCATGCTCTATTGT 15

RESULT 8

US-11-136-527-153312
;; Sequence 153312, Application US/11136527
;; Publication No. US20050287570A1
;; GENERAL INFORMATION:
;; APPLICANT: Wyeth
;; APPLICANT: Mounts, William M
;; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;; FILE REFERENCE: 031896-041000 (AM101086)
;; CURRENT APPLICATION NUMBER: US/11/136,527
;; CURRENT FILING DATE: 2005-05-25
;; PRIOR FILING DATE: 2005-05-26
;; PRIOR APPLICATION NUMBER: US 60/574,294
;; PRIOR FILING DATE: 2005-05-26
;; NUMBER OF SEQ ID NOS: 362830
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 153312
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: Probe
US-11-136-527-153312

Query Match 74.4%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GCATGCTCTATTGT 17
|||
Db 3 GCATGCTCTATTGT 17

RESULT 9

US-11-136-527-153313
;; Sequence 153313, Application US/11136527
;; Publication No. US20050287570A1
;; GENERAL INFORMATION:
;; APPLICANT: Wyeth
;; APPLICANT: Mounts, William M
;; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;; FILE REFERENCE: 031896-041000 (AM101086)
;; CURRENT APPLICATION NUMBER: US/11/136,527
;; CURRENT FILING DATE: 2005-05-25
;; PRIOR FILING DATE: 2005-05-26
;; PRIOR APPLICATION NUMBER: US 60/574,294
;; PRIOR FILING DATE: 2005-05-26
;; NUMBER OF SEQ ID NOS: 362830
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 153313
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: Probe

US-11-136-527-153313

Query Match 74.4%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GCATGCTCTATTGT 17
|||
Db 4 GCATGCTCTATTGT 18

RESULT 10

US-11-136-527-153317
;; Sequence 153317, Application US/11136527
;; Publication No. US20050287570A1
;; GENERAL INFORMATION:
;; APPLICANT: Wyeth
;; APPLICANT: Mounts, William M
;; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;; FILE REFERENCE: 031896-041000 (AM101086)
;; CURRENT APPLICATION NUMBER: US/11/136,527
;; CURRENT FILING DATE: 2005-05-25
;; PRIOR FILING DATE: 2005-05-26
;; PRIOR APPLICATION NUMBER: US 60/574,294
;; PRIOR FILING DATE: 2005-05-26
;; NUMBER OF SEQ ID NOS: 362830
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 153317
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: Probe
US-11-136-527-153317

Query Match 74.4%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GCATGCTCTATTGT 17
|||
Db 2 GCATGCTCTATTGT 16

RESULT 11

US-11-136-527-153325
;; Sequence 153325, Application US/11136527
;; Publication No. US20050287570A1
;; GENERAL INFORMATION:
;; APPLICANT: Wyeth
;; APPLICANT: Mounts, William M
;; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;; FILE REFERENCE: 031896-041000 (AM101086)
;; CURRENT APPLICATION NUMBER: US/11/136,527
;; CURRENT FILING DATE: 2005-05-25
;; PRIOR FILING DATE: 2005-05-26
;; PRIOR APPLICATION NUMBER: US 60/574,294
;; PRIOR FILING DATE: 2005-05-26
;; NUMBER OF SEQ ID NOS: 362830
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 153325
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: Probe
US-11-136-527-153325

Query Match 74.4%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GCATGCTCTATTGT 17
|||
Db 10 GCATGCTCTATTGT 24

RESULT 12
US-11-136-527-153326
; Sequence 153326, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 153326
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-153326

Query Match 74.4%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GCATGCTCTATTGT 17
| | | | | | | | | | | | | | | | | | | | |
Db 11 GCATGCTCTATTGT 25

RESULT 13
US-11-136-527-153341
; Sequence 153341, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 153341
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-153341

Query Match 74.4%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GCATGCTCTATTGT 17
| | | | | | | | | | | | | | | | | | | | |
Db 5 GCATGCTCTATTGT 19

RESULT 14
US-11-121-849-245961
; Sequence 245961, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 245961
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-245961

Query Match 73.3%; Score 13.2; DB 12; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGCATGCTCTATTGTA 18
| | | | | | | | | | | | | | | | | | | | |
Db 5 CGCATGCTCTATTGTA 22

RESULT 15
US-11-101-244-1437211/c
; Sequence 1437211, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1437211
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1437211

Query Match 72.2%; Score 13; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGCATGCTCTATT 14
| | | | | | | | | | | | | | | | | | | | |
Db 14 GGCATGCTCTATT 2

Search completed: March 4, 2006, 03:54:51
Job time : 447.711 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 4, 2006, 01:38:40 ; Search time 350.053 Seconds
(without alignment)
342.704 Million cell updates/sec

Title: US-09-701-583A-9

Perfect score: 18

Sequence: 1 cggcgtctctatttggta 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 4598950

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_21.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	2	AAQ78423 TGF-beta
2	18	100.0	18	3	Aaz65449 Immunosp
3	18	100.0	18	4	Aad18718 Human oli
4	18	100.0	18	14	Aeb01186 TGF-beta
5	18	100.0	22	3	Aaz65511 Immunosp
6	18	100.0	27	5	Aaf82681 Human TGF
7	16	88.9	16	3	Aaz65472 Immunosp
8	16	88.9	20	2	Aav48940 TGF-beta2
9	16	88.9	20	3	Aaz65448 Immunosp
10	16	88.9	20	3	Aaz65509 Immunosp
11	16	88.9	20	12	ADI80184 Human tra
12	16	88.9	20	12	ADI80039 Human tra
13	16	88.9	20	14	Aeb01185 TGF-beta
14	14.8	82.2	20	12	ADI80242 Mouse tra
15	14.8	82.2	20	12	ADI80115 Human tra
16	14.8	82.2	25	9	ACI91046 Human mic
17	14.4	80.0	17	2	AAZ3221 Integrin
18	14	77.8	17	2	AAZ3222 Integrin
19	14	77.8	20	12	ADI80053 Human tra

c	20	14	77.8	20	12	ADI80196	Adi80196 Human tra
	21	13.8	76.7	20	4	AAF59836	AAF59836 Human pro
	22	13.4	74.4	20	9	ADA74096	Ada74096 Equine la
	23	13.4	74.4	25	9	ACI55966	ACI55966 Human mic
c	24	13.4	74.4	30	14	AEI14421	Aeb114421 Plant lip
	25	13.2	73.3	25	9	ACK13008	ACK13008 Human mic
	26	13.2	73.3	25	9	ACK13010	ACK13010 Human mic
	27	13.2	73.3	25	9	ACI91047	ACI91047 Human mic
	28	13	72.2	17	2	AAZ3223	AAZ3223 Integrin
	29	12.8	71.1	20	12	ADP20509	ADP20509 Transcrip
c	30	12.8	71.1	22	3	AAC69355	AAC69355 Human ABC
	31	12.4	68.9	20	12	ADM33186	Adm33186 Oligo SEQ
	32	12.4	68.9	32	14	ADY71468	Ady71468 Trichinel
	33	12.4	68.9	37	12	ADQ26421	Adq26421 Brevibact
	34	12.4	68.9	37	13	ADR88316	ADR88316 Brevibact
c	35	12.2	67.8	18	3	AAZ76976	Aaz76976 Human bia
	36	12.2	67.8	18	12	ADQ81512	Adq81512 Synthetic
	37	12.2	67.8	18	12	ADQ81489	Adq81489 Synthetic
	38	12.2	67.8	18	12	ADQ81564	Adq81564 DNA oligo
	39	12.2	67.8	20	2	AAQ95371	Aaq95371 Primer A
	40	12.2	67.8	20	3	AAK99134	Aak99134 20-mer He
c	41	12.2	67.8	20	12	ADJ85601	Adj85601 Nucleic a
	42	12.2	67.8	23	9	ACF05388	Acf05388 Rat tumou
c	43	12.2	67.8	23	10	ADC83807	Adc83807 Human pap
	44	12.2	67.8	23	10	ADP43680	Adp43680 HPV 16 de
c	45	12.2	67.8	24	2	AAQ48628	Aaq48628 TNF-alpha

ALIGNMENTS

RESULT 1

AAQ78423

ID AAQ78423 standard; DNA; 18 BP.

XX AC: AAQ78423;

XX DT 25-MAR-2003 (revised)

XX DT 27-JUN-1995 (first entry)

XX TGF-beta gene phosphorothioate antisense oligonucleotide.

XX Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;

KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;

KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;

KW immunosuppression; oligonucleotide; ss.

XX OS Synthetic.

XX PN WO9425588-A2.

XX PD 10-NOV-1994.

XX PF 29-APR-1994; 94WO-EP001362.

XX PR 30-APR-1993; 93EP-00107089.

XX PR 13-MAY-1993; 93EP-00107849.

XX PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX PI Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;

XX PI Bogdahn U;

XX DR WPI; 1994-358266/44.

XX PT New transforming growth factor beta anti-sense oligo:nucleotide(s) - for

XX PT treating immunosuppression, tumours, etc.

XX PS Claim 6; Page 44; 74pp; English.

XX CC The antisense oligonucleotides are useful in the treatment of tumours in

XX CC which expression of TGF-beta is of relevance for pathogenicity and/or

XX CC inhibition of pathological angiogenesis. They are used especially for the

CC treatment of the immunosuppressive effect of TGF-beta, augmentation of
 CC the proliferation of cytotoxic lymphocytes, treatment of endogenous
 CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas
 CC and malignant gliomas, including glioblastomas, treatment and prophylaxis
 CC of skin carcinogenesis, and treatment of oesophageal and gastric
 CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESEQ files
 CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-
 CC beta 1. The sequences given in GENESEQ files AAQ78408-78487 are antisense
 CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
 CC analogues. (Updated on 25-MAR-2003 to correct PN field.)

XX
 SQ Sequence 18 BP; 3 A; 3 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCATGCTATTATTGTA 18
 |||||
 Db 1 CGGCATGCTATTATTGTA 18

RESULT 2

AAZ65449
 ID AAZ65449 standard; DNA; 18 BP.

XX
 AC AAZ65449;

XX
 DT 30-MAR-2000 (first entry)

XX
 DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-9.

XX
 KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
 KW vascular endothelial growth factor; VEGF; tumour; interleukin-10; IL-10; cancer;
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
 KW monocyte chemoattractant protein-1; MCP-1; ulcerative colitis; diabetes;
 KW glomerulonephritis; acute respiratory distress syndrome; ss;
 KW atherosclerosis.

XX
 OS Unidentified.

XX
 PN WO963975-A2.

XX
 PD 16-DEC-1999.

XX
 PF 10-JUN-1999; 99WO-BF004013.

XX
 PR 10-JUN-1998; 98EP-00110709.

XX
 PR 25-JUL-1998; 98EP-00113974.

XX
 PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX
 PI Schlingensiepen K, Schlingensiepen R, Brysch W;

XX
 DR WPI; 2000-097470/08.

XX
 PT Composition containing immune stimulant and inhibitor of agent that
 PT adversely affects the immune response, for treating cancers and
 PT infections.

XX
 PS Claim 5; Fig 1; 30pp; English.

XX
 CC This sequence is an immunosuppressant inhibitor oligonucleotide, which is
 CC used in the invention. The invention relates to a composition which
 CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.
 CC transforming growth factor TGF-beta, vascular endothelial growth factor
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
 CC that adversely affects the immune response. The composition also includes
 CC at least one stimulant that positively affects the immune response. This
 CC oligonucleotide is an example of an inhibitor that is used in the
 CC composition. The composition is used as an immunostimulant for the
 CC treatment of neoplasms and infections, particularly hyperproliferation;
 CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,

CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides
 CC most of which are directed against TGF-beta or VEGF, are inhibitors of
 CC monocyte chemoattractant protein-1 (MCP-1) and are useful as anti-
 CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress
 CC syndrome and the formation of atherosclerotic plaque

XX
 SQ Sequence 18 BP; 3 A; 3 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCATGCTATTATTGTA 18
 |||||
 Db 1 CGGCATGCTATTATTGTA 18

RESULT 3

AAID18718

ID AAD18718 standard; DNA; 18 BP.

XX
 AC AAD18718;

XX
 DT 18-DEC-2001 (first entry)

XX
 DE Human oligonucleotide #4, useful in drug target validation.

XX
 KW Human; TGF-beta; erbB-2; MIA; c-jun; junB; c-fos; VCAM; NF-kappaB p65;
 KW NF-kappaB p50; ICAM; VEGF; NF-kB 2; therapy; tumour; immune disorder;
 KW organ transplantation; cell expansion; drug target validation;
 KW antitumour; immunosuppressive; ss.

XX
 OS Homo sapiens.

XX
 PN EP1133988-A1.

XX
 PD 19-SEP-2001.

XX
 PF 11-MAR-2000; 2000EP-00105190.

XX
 PR 11-MAR-2000; 2000EP-00105190.

XX
 PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX
 PI Schlingensiepen K, Schlingensiepen R;

XX
 DR WPI; 2001-604124/69.

XX
 PT Mixture useful in preparation of medicament for treating tumors and
 PT immune disorders, comprises an inhibitor or suppressor of expression of a
 PT gene, and a molecule binding to expression product of the gene.

XX
 PS Claim 16; Page 2; 16pp; English.

XX
 CC The invention relates to a mixture comprising an inhibitor or suppressor
 CC of a gene and a molecule binding to an expression product of that gene.
 CC The gene is selected from the group consisting of TGF-beta, erbB-2, MIA,
 CC c-jun, junB, c-fos, VCAM, NF-kappaB p65, NF-kappaB p50, ICAM, VEGF and NF-
 CC -kB 2. Molecules including drugs are used to modulate biological
 CC functions through gene products and their derivatives - like e.g.
 CC glycosylated, phosphorylated or otherwise modified gene products, have
 CC either stimulated or inhibited gene products and/or their derivatives.
 CC The mixture is useful in the preparation of a medicament for treating
 CC tumours, immune disorders or for improving organ or cell transplantation
 CC or cell expansion, where inhibition of tumour growth, improvement of
 CC organ or cell transplantation or cell expansion and enhancement or
 CC inhibition of immune response is enhanced in a supra-additive manner. The
 CC mixture is useful in drug target validation, i.e., to identify genes that
 CC are relevant for certain pathological state by testing the effect of the
 CC mixture on a cell system or organism. The present sequence is a human

CC oligonucleotide useful in drug target validation
XX Sequence 18 BP; 3 A; 3 C; 4 G; 8 T; 0 U; 0 Other;
SQ Sequence 18 BP; 3 A; 3 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCATGCTCTATTGTGA 18
Db 1 CGGCATGCTCTATTGTGA 18

RESULT 4
AEB01186
ID AEB01186 standard; DNA; 18 BP.
XX AEB01186;
XX
XX
DT 08-SEP-2005 (first entry)
XX
DE TGF-beta 2 inhibition oligonucleotide SEQ ID NO 30.
XX
KW pharmaceutical; cell death; neoplasm; ss; Cytostatic; Apoptotic;
KW Immunostimulant; Antiarthritic; Antirheumatic; Antipsoriatic;
KW TGF-beta antagonist; Vaccine.
XX
XX Synthetic.
XX
XX WO2005059133-A2.
XX
XX 30-JUN-2005.
XX
XX 20-DEC-2004; 2004WO-EP053604.
XX
XX 19-DEC-2003; 2003EP-00029367.
XX 05-FEB-2004; 2004US-0541771P.
XX
XX (ANTI-) ANTISENSE PHARMA GMBH.
XX
XX Schlingensiepen K, Schlingensiepen R;
XX
XX WPI; 2005-479334/48.
XX
XX Pharmaceutical composition useful for treating neoplasm, comprises
PT stimulators stimulating function of immune system and/or immune cells and
PT substances inhibiting cell proliferation and/or inducing cell death.
XX
XX Claim 4; SEQ ID NO 30; 46pp; English.

CC The invention relates to a pharmaceutical composition (PC) comprising one
CC or more stimulators that stimulate the function of immune system and/or
CC immune cells and one or more substances inhibiting cell proliferation
CC and/or inducing cell death. A pharmaceutical composition is useful for
CC treating neoplasms chosen from solid tumors; blood born tumors such as
CC leukemia, acute or chronic myeloid or lymphoblastic leukemia; tumor
CC metastasis; benign tumors; or is chosen from bile duct carcinoma, bladder
CC carcinoma, brain tumor, breast carcinoma, bronchogenic carcinoma,
CC carcinoma of kidney, choriocarcinoma, cystadenocarcinoma, embryonal
CC carcinoma, epithelial carcinoma, esophageal carcinoma, cervical
CC carcinoma, colon carcinoma, colorectal carcinoma, endometrial carcinoma,
CC gallbladder carcinoma, gastric carcinoma, head and neck carcinoma, liver
CC carcinoma, lung carcinoma, medullary carcinoma, non-small cell
CC bronchogenic/lung carcinoma, ovarian carcinoma, pancreas carcinoma, small
CC papillary carcinoma, papillary adenocarcinoma, prostate carcinoma, small
CC intestine carcinoma, rectal carcinoma, renal cell carcinoma, skin
CC carcinoma, small-cell bronchogenic/lung carcinoma, squamous cell
CC carcinoma, sebaceous gland carcinoma, testicular carcinoma, uterine
CC carcinoma, rheumatoid arthritis and psoriasis. The present sequence
CC represents a TGF-beta 2 inhibition oligonucleotide.

XX
XX Sequence 18 BP; 3 A; 3 C; 4 G; 8 T; 0 U; 0 Other;
SQ Sequence 18 BP; 3 A; 3 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 26;

QY 1 CGGCATGCTCTATTGTGA 18
Db 1 CGGCATGCTCTATTGTGA 18

RESULT 5
AAZ65511
ID AAZ65511 standard; DNA; 22 BP.
XX AAZ65511;
XX
XX
DT 30-MAR-2000 (first entry)
XX
DE Immunosuppressant inhibitor oligonucleotide TGF-beta-12-9/22-2263.
XX
KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;
KW glomerulonephritis; acute respiratory distress syndrome; ss;
KW atherosclerosis.
XX
XX Unidentified.
XX
XX WO963975-A2.
XX
XX 16-DEC-1999.
XX
XX 10-JUN-1999; 99WO-EP04013.
XX
XX 10-JUN-1998; 98EP-00110709.
XX 25-JUL-1998; 98EP-00113974.
XX
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
XX Schlingensiepen K, Schlingensiepen R, Brysch W;
XX
XX WPI; 2000-097470/08.
XX
XX Composition containing immune stimulant and inhibitor of agent that
PT adversely affects the immune response, for treating cancers and
PT infections.
XX
XX Claim 10; Fig 1; 30pp; English.

CC This sequence is an immunosuppressant inhibitor oligonucleotide, which is
CC used in the invention. The invention relates to a composition which
CC contains at least one inhibitor (less than 100 kb) of a substance (e.g.
CC transforming growth factor TGF-beta, vascular endothelial growth factor
CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
CC that adversely affects the immune response. The composition also includes
CC at least one stimulant that positively affects the immune response. This
CC oligonucleotide is an example of an inhibitor that is used in the
CC composition. The composition is used as an immunostimulant for the
CC treatment of neoplasms and infections, particularly hyperproliferation;
CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
CC most of which are directed against TGFbeta or VEGF, are inhibitors of
CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative
CC colitis, diabetes, glomerulonephritis, acute respiratory distress
CC syndrome and the formation of atherosclerotic plaque

XX
XX Sequence 22 BP; 4 A; 3 C; 7 G; 8 T; 0 U; 0 Other;
SQ Sequence 22 BP; 4 A; 3 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 26;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCATGCTCTATTGTGA 18
| | | | | | | | | | | | | | | | | |
Db 5 CGGCATGCTCTATTGTGA 22

RESULT 6

AAF82681

ID AAF82681 standard; DNA; 27 BP.

XX AAF82681;

AC AAF82681;

XX 18-JUN-2001 (first entry)

DT Human TGF-beta2 PCR primer #2.

XX Human; androgen response element; ARE; cytostatic; gene therapy;

XX prostate-specific chimeric enhancer; transcriptional regulation;

XX targeted gene expression; prostate cancer; prostate disorder;

XX prostate-specific antigen; PSA; transforming growth factor beta2;

XX TGF-beta2; PCR primer; ss.

XX Homo sapiens.

OS W0200127256-A2.

XX 19-APR-2001.

XX 13-OCT-2000; 2000WO-US028444.

XX 14-OCT-1999; 99US-0159691P.

XX 15-OCT-1999; 99US-0159730P.

XX (REGC) UNIV CALIFORNIA SYSTEM.

XX Wu L, Carey MF, Belldgrun AS;

XX WPI; 2001-273768/28.

XX New polynucleotide, useful for treating prostatic cancer, comprises

XX prostate specific chimeric enhancer and proximal promoter sequence

XX operably linked to nucleic acid encoding heterologous polypeptide.

XX Example 5; Page 73; 131pp; English.

XX The present sequence was used in reverse transcriptase polymerase chain

XX reaction (RT-PCR) analysis of human prostate cancer cells. The invention

XX relates to an isolated polynucleotide comprising a prostate-specific

XX chimeric enhancer (PSE) sequence and a proximal promoter sequence

XX operably linked to a nucleic acid segment that encodes a heterologous

XX polypeptide. The PSE contains an ARE and specifically activates

XX transcription of the nucleic acid segment in a mammalian prostate cell.

XX The construct is useful for the treatment of a prostate disorder or a

XX metastasized prostate cancer, such as hyperplasia or hyperproliferation

XX of prostate cells. It is also useful for directing the tissue-specific

XX expression of a heterologous polypeptide in a human prostate cell. The

XX construct may be administered by injection, infection, transformation,

XX liposome-mediated transfection, polybrene-mediated transfection, receptor

XX -mediated uptake or Ca-PO4-mediated transformation

XX Sequence 27 BP; 5 A; 7 C; 6 G; 9 T; 0 U; 0 Other;

SQ Query Match 100.0%; Score 18; DB 5; Length 27;

Best Local Similarity 100.0%; Pred. No. 27;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCATGCTCTATTGTGA 18

| | | | | | | | | | | | | | | | | |

Db 3 CGGCATGCTCTATTGTGA 20

RESULT 7

AAZ65472
ID AAZ65472 standard; DNA; 16 BP.

XX AAZ65472;

AC AAZ65472;

XX 30-MAR-2000 (first entry)

DT Immunosuppressant inhibitor oligonucleotide TGF-beta2-9/1.

XX Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;

XX vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;

XX prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;

XX monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;

XX glomerulonephritis; acute respiratory distress syndrome; ss;

XX atherosclerosis.

XX Unidentified.

OS WO9963975-A2.

XX 16-DEC-1999.

XX 10-JUN-1999; 99WO-EF004013.

XX 10-JUN-1998; 98EP-00110709.

XX 25-JUL-1998; 98EP-00113974.

XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX Schlingensiepen K, Schlingensiepen R, Brysch W;

XX WPI; 2000-097470/08.

XX Composition containing immune stimulant and inhibitor of agent that

XX adversely affects the immune response, for treating cancers and

XX infections.

XX Claim 5; Fig 1; 30pp; English.

XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is

XX used in the invention. The invention relates to a composition which

XX contains at least one inhibitor (less than 100 kD) of a substance (e.g.

XX transforming growth factor TGF-beta, vascular endothelial growth factor

XX VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)

XX that adversely affects the immune response. The composition also includes

XX at least one stimulant that positively affects the immune response. This

XX oligonucleotide is an example of an inhibitor that is used in the

XX composition. The composition is used as an immunostimulant for the

XX treatment of neoplasms and infections, particularly hyperproliferation;

XX leukaemia, (non-)Hodgkin's lymphoma, carcinoma (of oesophagus, bronchi,

XX colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,

XX breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,

XX malignant melanoma, brain tumours and sarcomas. The oligonucleotides,

XX most of which are directed against TGFbeta or VEGF, are inhibitors of

XX monocyte chemotactic protein-1 (MCP-1) and are useful as anti-

XX inflammatory for treating e.g. asthma, Crohn's disease, ulcerative

XX colitis, diabetes, glomerulonephritis, acute respiratory distress

XX syndrome and the formation of atherosclerotic plaque

XX Sequence 16 BP; 2 A; 3 C; 4 G; 7 T; 0 U; 0 Other;

SQ Query Match 88.9%; Score 16; DB 3; Length 16;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCATGCTCTATTGTG 16

| | | | | | | | | | | | | | | |

Db 1 CGGCATGCTCTATTGTG 16

RESULT 8

AAV48940

ID AAV48940 standard; DNA; 20 BP.

DE Immunosuppressant inhibitor oligonucleotide TGF-beta-12-9/20-2261.
XX
XX Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
KW monocyte chemoattractant protein-1; MCP-1; ulcerative colitis; diabetes;
KW glomerulonephritis; acute respiratory distress syndrome; ss;
KW atherosclerosis.
XX
XX Unidentified.
OS
XX
XX
XX
XX W09963975-A2.
XX
XX 16-DEC-1999.
XX
XX 10-JUN-1999; 99WO-EP004013.
XX
XX 10-JUN-1998; 98EP-00110709.
PR 25-JUL-1998; 98EP-00113974.
XX
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
PA
XX Schlingensiepen K, Schlingensiepen R, Brysch W;
PI
XX WPI; 2000-097470/08.
DR
XX
XX Composition containing immune stimulant and inhibitor of agent that
PT adversely affects the immune response, for treating cancers and
PT infections.
PT
XX
XX Claim 10; Fig 1; 30pp; English.
PS
XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is
CC used in the invention. The invention relates to a composition which
CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.
CC transforming growth factor TGF-beta, vascular endothelial growth factor
CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
CC that adversely affects the immune response. The composition also includes
CC at least one stimulant that positively affects the immune response. This
CC oligonucleotide is an example of an inhibitor that is used in the
CC composition. The composition is used as an immunostimulant for the
CC treatment of neoplasms and infections, particularly hyperproliferation;
CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides
CC most of which are directed against TGFbeta or VEGF, are inhibitors of
CC monocyte chemoattractant protein-1 (MCP-1) and are useful as anti-
CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative
CC colitis, diabetes, glomerulonephritis, acute respiratory distress
CC syndrome and the formation of atherosclerotic plaque
XX
XX
SQ Sequence 20 BP; 3 A; 3 C; 7 G; 7 T; 0 U; 0 Other;
Query Match 88.9%; Score 16; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 5 CGGCATGCTCTATTG 20
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XX
XX ADI80184;
AC
XX
XX 22-APR-2004 (first entry)
DT
XX
XX Human transforming growth factor-beta 2 target DNA region, SEQ ID No 185.

KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; human.
XX
OS Homo sapiens.
XX
XX US2004006030-A1.
XX
XX 08-JAN-2004.
XX
XX 02-JUL-2002; 2002US-00189267.
XX
XX 02-JUL-2002; 2002US-00189267.
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX Monia BP, Freier SM, Dobie KW;
PI
XX WPI; 2004-081742/08.
DR
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
PT
XX
XX Example 16; SEQ ID NO 185; 135pp; English.
PS
XX
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX
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Query Match 88.9%; Score 16; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 16 CGGCATGCTCTATTG 1
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ID ADI80039 standard; DNA; 20 BP.
XX
XX ADI80039;
AC
XX
XX 22-APR-2004 (first entry)
DT
XX
XX Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 40.
XX
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;


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XX 02-JUL-2002; 2002US-00189267.
PF
XX
XX 02-JUL-2002; 2002US-00189267.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Monia BP, Freier SM, Dobie KW;
PI
XX
XX WPI; 2004-081742/08.
DR
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
PT
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT
XX neurodegenerative disorder, or a disease involving hyperactivation of
PT
XX immune response.
XX
XX Example 16; SEQ ID NO 243; 135pp; English.
PS
XX
XX The invention relates to a novel antisense compound of 8-80 nucleobases
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XX in length targeted to, and which specifically hybridizes with, a nucleic
CC
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC
XX inhibits the expression of TGF-beta 2. The invention further relates to:
CC
XX a compound 8-80 nucleobases in length that specifically hybridizes with
CC
XX at least an 8-nucleobase portion of an active site on a nucleic acid
CC
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
CC
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC
XX tissues by contacting the cells or tissues with the compound so that
CC
XX expression of TGF-beta 2 is inhibited; treating an animal having a
CC
XX disease or condition associated with TGF-beta 2 by administering to the
CC
XX animal a therapeutic or prophylactic amount of the compound so that
CC
XX expression of TGF-beta 2 is inhibited; and screening an antisense
CC
XX compound. The antisense compound has cytostatic, neurotropic,
CC
XX neuroprotective, and immunosuppressive activities. The compound,
CC
XX composition and methods are useful for treating a disease or condition
CC
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC
XX cancer, a neurodegenerative disorder, or a disease or condition involving
CC
XX hyperactivation of an immune response. This polynucleotide sequence
CC
XX represents a preferred target DNA region of TGF-beta 2 of the invention.
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XX AC ADI80115;
XX
XX DT 22-APR-2004 (first entry)
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XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 116.
XX
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX
XX OS Mus musculus.
XX
XX PN US2004006030-A1.
XX
XX PD 08-JAN-2004.
XX
XX PF 02-JUL-2002; 2002US-00189267.
XX
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PR 02-JUL-2002; 2002US-00189267.
XX (ISIS-) ISIS PHARM INC.
PA
XX Monia BP, Freier SM, Dobie KW;
PI
XX
XX WPI; 2004-081742/08.
DR
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
PT
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT
XX neurodegenerative disorder, or a disease involving hyperactivation of
PT
XX immune response.
XX
XX Example 16; SEQ ID NO 116; 135pp; English.
PS
XX
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC
XX in length targeted to, and which specifically hybridizes with, a nucleic
CC
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC
XX inhibits the expression of TGF-beta 2. The invention further relates to:
CC
XX a compound 8-80 nucleobases in length that specifically hybridizes with
CC
XX at least an 8-nucleobase portion of an active site on a nucleic acid
CC
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
CC
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC
XX tissues by contacting the cells or tissues with the compound so that
CC
XX expression of TGF-beta 2 is inhibited; treating an animal having a
CC
XX disease or condition associated with TGF-beta 2 by administering to the
CC
XX animal a therapeutic or prophylactic amount of the compound so that
CC
XX expression of TGF-beta 2 is inhibited; and screening an antisense
CC
XX compound. The antisense compound has cytostatic, neurotropic,
CC
XX neuroprotective, and immunosuppressive activities. The compound,
CC
XX composition and methods are useful for treating a disease or condition
CC
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC
XX cancer, a neurodegenerative disorder, or a disease or condition involving
CC
XX hyperactivation of an immune response. This polynucleotide sequence
CC
XX represents an antisense oligonucleotide of the invention.
XX
XX Sequence 20 BP; 6 A; 3 C; 4 G; 7 T; 0 U; 0 Other;
SQ
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XX Query Match 82.2%; Score 14.8; DB 12; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 1.1e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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XX Db 1 CGGCATGCTGATTATATA 18
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OM nucleic - nucleic search, using sw model

Run on: March 4, 2006, 01:42:16 ; Search time 957.368 Seconds
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	20	100.0	20	6 A90351	A90351 Sequence 53
3	20	100.0	20	6 BD065897	BD065897 An antise
4	20	100.0	20	6 BD234910	BD234910 A method
5	20	100.0	20	6 CS123684	CS123684 Sequence
6	20	100.0	20	6 AX008981	AX008981 Sequence
7	20	100.0	20	6 AX252495	AX252495 Sequence
8	18	90.0	18	6 A89125	A89125 Sequence 12
9	18	90.0	18	6 BD066638	BD066638 An antise
10	18	90.0	18	6 BD234924	BD234924 A method
11	18	90.0	18	6 AX008995	AX008995 Sequence
12	16	80.0	16	6 A89127	A89127 Sequence 12
13	16	80.0	16	6 BD066640	BD066640 An antise
14	16	80.0	16	6 BD234926	BD234926 A method
15	16	80.0	16	6 AX008997	AX008997 Sequence
16	16	80.0	18	6 A40542	A40542 Sequence 79
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23	16	80.0	18	6 AX030117	AX030117 Sequence
24	16	80.0	18	6 AX316438	AX316438 Sequence
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27	15	75.0	15	6 BD234925	BD234925 A method
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35	13.2	66.0	20	6 CS116412	CS116412 Sequence
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38	13.2	66.0	20	6 AX785541	AX785541 Sequence
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ALIGNMENTS

RESULT 1
LOCUS A88384 A88384 20 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 532 from Patent WO9833904.
ACCESSION A88384
VERSION A88384.1 GI:6736954
KEYWORDS
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Brysch, W. and Schlingensiepen, K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 532 06-AUG-1998;
BIOGNOSTIK GBS (DE); BRYSCH WOLFGANG (DE)
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DEFINITION Sequence 532 from Patent EP0856579.
ACCESSION A90351
VERSION A90351.1 GI:6738865
KEYWORDS
SOURCE unidentified
ORGANISM unclassified sequences.

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REFERENCE 1 (bases 1 to 20)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 532 03-AUG-1998;
BIOGNOSTIK GES (DE)
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DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065897
VERSION BD065897.1 GI:22611500
KEYWORDS JP 2001511000-A/532.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 532 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/532
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
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LOCUS 20 bp DNA linear PAT 17-JUL-2003
DEFINITION A method for stimulating the immune system.
ACCESSION BD234910
VERSION BD234910.1 GI:130404680
KEYWORDS JP 2002517434-A/14.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 20)
AUTHORS Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
TITLE A method for stimulating the immune system
JOURNAL Patent: JP 2002517434-A 14 18-JUN-2002;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Homo sapiens (human)
PN JP 2002517434-A/14
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PI KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
PC 00,A61P35/00,
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DEFINITION Sequence 35 from Patent WO2005059133.
ACCESSION CS123684
VERSION CS123684.1 GI:70912177
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Schlingensiepen,K.H.
TITLE Combination therapy associating a tgf-beta antagonist with a
chemotherapeutic agent
JOURNAL Patent: WO 2005059133-A 35 30-JUN-2005;
Antisense Pharma GmbH (DE)
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LOCUS AX008981 20 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 14 from Patent WO9963975.
ACCESSION AX008981
VERSION AX008981.1 GI:9996355
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 Brysch, W., Schlingensiepen, K.H. and Schlingensiepen, R.
AUTHORS A method for stimulating the immune system
TITLE Patent: WO 9963975-A 14 16-DEC-1999;
JOURNAL BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
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DEFINITION Sequence 5 from Patent WO0168146.
ACCESSION AX252495
VERSION AX252495.1 GI:15985766
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 Schlingensiepen, K.H. and Schlingensiepen, R.
AUTHORS Mixture comprising an inhibitor or suppressor of a gene and a
TITLE molecule binding to an expression product of that gene
JOURNAL Patent: WO 0168146-A 5 20-SEP-2001;
Biognostik Gesellschaft fuer biomolekulare Diagnostik mbH (DE)
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DEFINITION Sequence 1273 from Patent WO9833904.
ACCESSION A89125
VERSION A89125.1 GI:6737695
KEYWORDS

SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 18)
AUTHORS Brysch, W. and Schlingensiepen, K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1273 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066638
VERSION BD066638.1 GI:22612241
KEYWORDS JP 2001511000-A/1273.
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen, K.H. and Brysch, W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1273 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/1273
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PI 31-JAN-1997 EP 97101531.8
PC C12N15/11, C07H21/04, A61K31/70
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Matches 18; Conservative 0;
QY 2 CTTTCACCAAAATTGGAAG 19
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Db 1 CTTTCACCAAAATTGGAAG 18
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BD234924
LOCUS BD234924 18 bp DNA linear PAT 17-JUL-2003
DEFINITION A method for stimulating the immune system.
ACCESSION BD234924
VERSION BD234924.1 GI:33044694
KEYWORDS JP 2002517434-A/28.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
TITLE A method for stimulating the immune system
JOURNAL Patent: JP 2002517434-A 28 JUN-2002;
COMMENT BIOLOGIST GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
PN JP 2002517434-A/28
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
PC 00,A61P35/00.
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
method for stimulating the immune system
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CTTTCACCAAAATGGGAAG 19
DB 1 CTTTCACCAAAATGGGAAG 18
RESULT 11
AX008995
LOCUS Homo sapiens 18 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 28 from Patent WO9963975.
ACCESSION AX008995
VERSION AX008995.1 GI:9996369
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1
AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE A method for stimulating the immune system
JOURNAL Patent: WO 9963975-A 28 DEC-1999;
BIOLOGIST GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 CTTTCACCAAAATGGGAAG 18

RESULT 12
A89127
LOCUS Homo sapiens 16 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1275 from Patent WO9833904.
ACCESSION A89127
VERSION A89127.1 GI:6737697
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified sequences.
REFERENCE 1 (bases 1 to 16)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1275 06-AUG-1998;
BIOLOGIST GES (DE); BRYSCH WOLFGANG (DE)
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QY 5 TCACCAAAATGGGAAGC 20
DB 1 TCACCAAAATGGGAAGC 16
RESULT 13
BD066640
LOCUS Homo sapiens 16 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066640
VERSION BD066640.1 GI:22612243
KEYWORDS JP 2001511000-A/1275.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1275 07-AUG-2001;
BIOLOGIST GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/1275
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
FT source 1..16
FT Location/Qualifiers
/organism="Unknown".
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source
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 80.0%; Score 16; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.1e+03; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TCACCAAAATGGGAAGC 20
DB 1 TCACCAAAATGGGAAGC 16

RESULT 14

BD234926
 LOCUS
 DEFINITION A method for stimulating the immune system.
 ACCESSION
 VERSION BD234926.1 GI:33044696
 KEYWORDS JP 2002517434-A/30.
 SOURCE Homo sapiens (human)
 ORGANISM

REFERENCE

AUTHORS Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
 TITLE A method for stimulating the immune system
 JOURNAL Patent: JP 2002517434-A 30 18-JUN-2002;
 COMMENT BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
 OS Homo sapiens (human)
 PN JP 2002517434-A/30
 PD 18-JUN-2002
 PF 10-JUN-1999 JP 2000553044
 PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
 KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
 BRYSCH

PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
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 PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
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 FH Key Location/Qualifiers
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FEATURES
source

ORIGIN

Query Match 80.0%; Score 16; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 TCACCAAAATTGGAAGC 20
 DB 1 TCACCAAAATTGGAAGC 16

RESULT 15

AX008997
 LOCUS
 DEFINITION Sequence 30 from Patent WO9963975.
 ACCESSION AX008997
 VERSION AX008997.1 GI:9996371
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE

AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
 TITLE A method for stimulating the immune system
 JOURNAL Patent: WO 9963975-A 30 16-DEC-1999;
 BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
 HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)

FEATURES
source

1..16
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 /mol_type='unassigned DNA'
 /db_xref='taxon:9606'

ORIGIN

Query Match 80.0%; Score 16; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 TCACCAAAATTGGAAGC 20
 DB 1 TCACCAAAATTGGAAGC 16

Search completed: March 4, 2006, 10:47:49
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OM nucleic - nucleic search, using sw model

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Title: US-09-701-583A-14

Perfect score: 20

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Scoring table: IDENTITY_NUC

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Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 4598950

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: Geneseqn1980s.*

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3: Geneseqn2000s.*

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6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	20	100.0	20	2	AAV48943
2	20	100.0	20	3	AAZ65454
3	20	100.0	20	4	AAAD18719
4	20	100.0	20	14	AEb01191
5	18	90.0	18	3	AAZ65468
6	18	90.0	20	12	ADI80035
7	18	90.0	20	12	ADI80181
8	16	80.0	16	3	AAZ65470
9	16	80.0	18	2	AAQ78430
10	16	80.0	18	3	AAZ65453
11	16	80.0	18	14	AEb01190
12	15	75.0	15	3	AAZ65469
13	14.2	71.0	20	8	AAU48552
14	14.2	71.0	20	12	ADK78448
15	14.2	71.0	20	12	ADK78529
16	14.2	71.0	24	6	ABZ25543
17	14.2	71.0	32	2	AAV72954
18	14.2	71.0	40	12	ADP71056
19	13.8	69.0	17	4	AAH95671

C	20	13.8	69.0	19	10	ADF92715
C	21	13.8	69.0	19	10	ADF92603
C	22	13.8	69.0	29	3	AAA04270
C	23	13.8	69.0	37	9	ACF57163
C	24	13.8	69.0	40	13	ADU50752
C	25	13.8	69.0	40	13	ADU50751
C	26	13.6	68.0	33	6	ABX14388
C	27	13.2	66.0	20	4	ADI14558
C	28	13.2	66.0	20	10	ADD42186
C	29	13.2	66.0	20	10	ADD42188
C	30	13.2	66.0	20	10	ADD42190
C	31	13.2	66.0	20	10	ADD93796
C	32	13.2	66.0	20	12	ADK77402
C	33	13.2	66.0	20	12	ADK74986
C	34	13.2	66.0	20	14	AEA13360
C	35	13.2	66.0	21	9	ACH03553
C	36	13.2	66.0	22	8	ACC62420
C	37	13.2	66.0	23	10	ACF36660
C	38	13.2	66.0	23	12	ADJ93569
C	39	13.2	66.0	24	2	AAQ45017
C	40	13.2	66.0	24	2	AAV42144
C	41	13.2	66.0	24	2	AAV67008
C	42	13.2	66.0	24	6	ABQ09564
C	43	13.2	66.0	24	6	ABQ02831
C	44	13.2	66.0	24	6	ABQ09605
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ALIGNMENTS

RESULT 1

AAV48943

ID AAV48943 standard; DNA; 20 BP.

XX AC AAV48943;

XX DT 15-OCT-1998 (first entry)

XX DE TGF-beta2 antisense oligonucleotide TGF-beta2-14.

XX DE TGF-beta2 antisense oligonucleotide TGF-beta2-14.

XX DE TGF-beta2 antisense oligonucleotide TGF-beta2-14.

XX DE TGF-beta2 antisense oligonucleotide TGF-beta2-14.

XX DE TGF-beta2 antisense oligonucleotide TGF-beta2-14.

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XX DE TGF-beta2 antisense oligonucleotide TGF-beta2-14.

XX DE TGF-beta2 antisense oligonucleotide TGF-beta2-14.

XX DE TGF-beta2 antisense oligonucleotide TGF-beta2-14.

Preparation of antisense oligonucleotide(s) which lack long runs of consecutive guanosine or inosine - and have specific ratio of residues able to form two or three hydrogen bonds, have greater activity and reduced toxicity, used therapeutically or to modulate growth of cells in culture.

Claim 10; Fig 8a; 286pp; English.

AAV48930-49007 represent antisense oligonucleotides directed against transforming growth factor-beta2 (TGF-beta2). Of these, only oligonucleotides AAV48930-67 resulted in significant reduction in TGF-beta 2 protein expression, while oligonucleotides AAV48968-49007 had

CC little effect. The oligonucleotides exemplify the invention. The
 CC specification describes oligonucleotides that contain 8-30 nucleotides,
 CC which contain at most 8 nucleotides that can each form three hydrogen
 CC bonds to cytosine; do not contain four consecutive nucleotides able to
 CC form three H-bonds each to four consecutive cytosines; do not contain two
 CC sequences of three consecutive nucleotides each able to form three H-
 CC bonds to three consecutive cytosines, and the ratio between residues able
 CC to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R
 CC = 0.33-0.72. The oligonucleotides are used to modulate expression of
 CC genes, particularly the genes for p53, ErbB-2, JunB, JunD, TGF-beta 1 or
 CC beta 2 to control proliferation of primary cell cultures (e.g. bone
 CC marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or
 CC keratinocytes). The oligonucleotides can also be used to analyse function
 CC of proteins (by altering their expression or activity) and
 CC therapeutically, e.g. in cases of cancer or (targeting TGF) for
 CC stimulating the immune system

XX Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTCACCAAAATGGAAGC 20
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 DB 1 GCTTTCACCAAAATGGAAGC 20

RESULT 2

AAZ65454
 ID AAZ65454 standard; DNA; 20 BP.

XX AC AAZ65454;

XX DT 30-MAR-2000 (first entry)

XX DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-14.

XX KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
 KW monocyte chemoattractant protein-1; MCP-1; ulcerative colitis; diabetes;
 KW glomerulonephritis; acute respiratory distress syndrome; ss;
 KW atherosclerosis.

XX OS Unidentified.

XX PN WO963975-A2.

XX PD 16-DEC-1999.

XX PF 10-JUN-1999; 99WO-EP004013.

XX PR 10-JUN-1998; 98EP-00110709.

XX PR 25-JUL-1998; 98EP-00113974.

XX PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX PI Schlingensiepen K, Schlingensiepen R, Brysch W;

XX DR WPI; 2000-097470/08.

XX PT Composition containing immune stimulant and inhibitor of agent that
 PT adversely affects the immune response, for treating cancers and
 PT infections.

XX PS Claim 5; Fig 1; 30pp; English.

XX CC This sequence is an immunosuppressant inhibitor oligonucleotide, which is
 CC used in the invention. The invention relates to a composition which
 CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.
 CC transforming growth factor TGF-beta, vascular endothelial growth factor
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)

CC that adversely affects the immune response. The composition also includes
 CC at least one stimulant that positively affects the immune response. This
 CC oligonucleotide is an example of an inhibitor that is used in the
 CC composition. The composition is used as an immunostimulant for the
 CC treatment of neoplasms and infections, particularly hyperproliferation;
 CC leukaemia; (non-Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
 CC most of which are directed against TGFbeta or VEGF, are inhibitors of
 CC monocyte chemoattractant protein-1 (MCP-1) and are useful as anti-
 CC inflammatories for treating e.g. asthma, Crohn's disease, ulcerative
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress
 CC syndrome and the formation of atherosclerotic plaque

XX Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTCACCAAAATGGAAGC 20
 |||||
 DB 1 GCTTTCACCAAAATGGAAGC 20

RESULT 3

AAAD18719

ID AAD18719 standard; DNA; 20 BP.

XX AC AAD18719;

XX DT 18-DEC-2001 (first entry)

XX DE Human oligonucleotide #5, useful in drug target validation.

XX KW Human; TGF-beta; erbB-2; MIA; c-jun; junB; c-fos; VCAM; NF-kappaB p65;
 KW NF-kappaB p50; ICAM; VEGF; NF-kB 2; therapy; tumour; immune disorder;
 KW organ transplantation; cell expansion; drug target validation;
 KW antitumour; immunosuppressive; ss.

XX OS Homo sapiens.

XX PN EP1133988-A1.

XX PD 19-SEP-2001.

XX PF 11-MAR-2000; 2000EP-00105190.

XX PR 11-MAR-2000; 2000EP-00105190.

XX PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX PI Schlingensiepen K, Schlingensiepen R;

XX DR WPI; 2001-604124/69.

XX PT Mixture useful in preparation of medicament for treating tumors and
 PT immune disorders, comprises an inhibitor or suppressor of expression of a
 PT gene, and a molecule binding to expression product of the gene.

XX PS Claim 16; Page 3; 16pp; English.

XX CC The invention relates to a mixture comprising an inhibitor or suppressor
 CC of a gene and a molecule binding to an expression product of that gene.
 CC The gene is selected from the group consisting of TGF-beta, erbB-2, MIA,
 CC c-jun, junB, c-fos, VCAM, NF-kappaB p65, NF-kappaB p50, ICAM, VEGF and NF
 CC -kB 2. Molecules including drugs are used to modulate biological
 CC functions through gene products and their derivatives - like e.g.
 CC glycosylated, phosphorylated or otherwise modified gene products, have
 CC either stimulated or inhibited gene products and/or their derivatives.
 CC The mixture is useful in the preparation of a medicament for treating
 CC tumours, immune disorders or for improving organ or cell transplantation

CC or cell expansion, where inhibition of tumour growth, improvement of
 CC organ or cell transplantation or cell expansion and enhancement or
 CC inhibition of immune response is enhanced in a supra-additive manner. The
 CC mixture is useful in drug target validation, i.e., to identify genes that
 CC are relevant for certain pathological state by testing the effect of the
 CC mixture on a cell system or organism. The present sequence is a human
 CC oligonucleotide useful in drug target validation

XX Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;

Best Local Similarity 100.0%; Pred. No. 4.3; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0;

Oy 1 GCTTTCCACCAATTTGGAAGC 20

Db 1 GCTTTCCACCAATTTGGAAGC 20

RESULT 4

AEBO1191

ID AEB01191 standard; DNA; 20 BP.

AC AEB01191;

XX 08-SEP-2005 (first entry)

DT TGF-beta 2 inhibition oligonucleotide SEQ ID NO 35.

DE Pharmaceutical; cell death; neoplasm; ss; Cytostatic; Apoptotic;

XX Immunostimulant; Antiarthritic; Antirheumatic; Antipsoriatic;

KW TGF-beta antagonist; Vaccine.

XX Synthetic.

OS WO2005059133-A2.

XX 30-JUN-2005.

PD 20-DEC-2004; 2004WO-EP053604.

PF 19-DEC-2003; 2003EP-00029367.

XX 05-FEB-2004; 2004US-0541771P.

PR (ANTI-) ANTISENSE PHARMA GMBH.

XX Schlingensiepen K, Schlingensiepen R;

PI WPI; 2005-479334/48.

DR Pharmaceutical composition useful for treating neoplasm, comprises

XX stimulators stimulating function of immune system and/or immune cells and

PT substances inhibiting cell proliferation and/or inducing cell death.

XX Claim 4; SEQ ID NO 35; 46pp; English.

PS The invention relates to a pharmaceutical composition (PC) comprising one

XX or more stimulators that stimulate the function of immune system and/or

CC immune cells and one or more substances inhibiting cell proliferation

CC and/or inducing cell death. A pharmaceutical composition is useful for

CC treating neoplasms chosen from solid tumors; blood born tumors such as

CC leukemias, acute or chronic myeloid or lymphoblastic leukemia; tumor

CC metastasis; benign tumors; or is chosen from bile duct carcinoma; bladder

CC carcinoma; brain tumor; breast carcinoma; bronchogenic carcinoma;

CC carcinoma of kidney; choriocarcinoma, cystadenocarcinoma, embryonal

CC carcinoma, epithelial carcinoma, esophageal carcinoma, cervical

CC carcinoma, colon carcinoma, colorectal carcinoma, endometrial carcinoma,

CC gallbladder carcinoma, gastric carcinoma, head and neck carcinoma, liver

CC carcinoma, lung carcinoma, medullary carcinoma, non-small cell

CC bronchogenic/lung carcinoma, ovarian carcinoma, pancreas carcinoma,

CC papillary carcinoma, papillary adenocarcinoma, prostate carcinoma, small

CC intestine carcinoma, rectal carcinoma, renal cell carcinoma, skin

CC carcinoma, small-cell bronchogenic/lung carcinoma, squamous cell

CC carcinoma, sebaceous gland carcinoma, testicular carcinoma, uterine

CC carcinoma, rheumatoid arthritis and psoriasis. The present sequence

XX represents a TGF-beta 2 inhibition oligonucleotide.

SQ Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 20;

Best Local Similarity 100.0%; Pred. No. 4.3; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0;

Oy 1 GCTTTCCACCAATTTGGAAGC 20

Db 1 GCTTTCCACCAATTTGGAAGC 20

RESULT 5

AAZ65468

ID AAZ65468 standard; DNA; 18 BP.

XX AAZ65468;

AC 30-MAR-2000 (first entry)

XX Immunosuppressant inhibitor oligonucleotide TGF-beta2-14/1.

DE Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;

XX vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;

KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;

XX monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;

KW glomerulonephritis; acute respiratory distress syndrome; ss;

XX atherosclerosis.

XX Unidentified.

OS WO9963975-A2.

XX 16-DEC-1999.

PD 10-JUN-1999; 99WO-EP004013.

PF 10-JUN-1998; 98EP-00110709.

XX 25-JUL-1998; 98EP-00113974.

PR (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX Schlingensiepen K, Schlingensiepen R, Brysch W;

PI WPI; 2000-097470/08.

DR Composition containing immune stimulant and inhibitor of agent that

XX adversely affects the immune response, for treating cancers and

PT infections.

XX Claim 5; Fig 1; 30pp; English.

PS This sequence is an immunosuppressant inhibitor oligonucleotide, which is

XX used in the invention. The invention relates to a composition which

CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.

CC transforming growth factor TGF-beta, vascular endothelial growth factor

CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)

CC that adversely affects the immune response. The composition also includes

CC at least one stimulant that positively affects the immune response. This

CC oligonucleotide is an example of an inhibitor that is used in the

CC composition. The composition is used as an immunostimulant for the

CC treatment of neoplasms and infections, particularly hyperproliferation;

CC leukaemia; (non-Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,

CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,

CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,

CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,

CC most of which are directed against TGFbeta or VEGF, are inhibitors of

CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-

CC inflammatories for treating e.g. asthma, Crohn's disease, ulcerative

CC colitis, diabetes, glomerulonephritis, acute respiratory distress

CC syndrome and the formation of atherosclerotic plaque

XX Sequence 18 BP; 6 A; 4 C; 3 G; 5 T; 0 U; 0 Other;

SQ Sequence 18 BP; 6 A; 4 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 90.0%; Score 18; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 43;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTTCACCAAAATGGGAAG 19

DB 1 CTTTCACCAAAATGGGAAG 18

RESULT 6

ADI80035

ID ADI80035 standard; DNA; 20 BP.

XX AC

XX ADI80035;

DT 22-APR-2004 (first entry)

XX DE

XX Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 36.

XX KW

XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;

KW cytostatic; neurotropic; neuroprotective; immunosuppressive;

KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;

KW immune; ss; human.

XX OS

XX Homo sapiens.

XX PN

XX US2004006030-A1.

XX PD

XX 08-JAN-2004.

XX PF

XX 02-JUL-2002; 2002US-00189267.

XX PR

XX 02-JUL-2002; 2002US-00189267.

XX PA

XX (ISIS-) ISIS PHARM INC.

XX PI

XX Monia BP, Freier SM, Dobie KW;

XX DR

XX WPI; 2004-081742/08.

XX PT

XX New compounds, particularly antisense oligonucleotides targeted to a

PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a

PT neurodegenerative disorder, or a disease involving hyperactivation of

PT immune response.

XX PS

XX Example 15; SEQ ID NO 36; 135pp; English.

XX CC

XX The invention relates to a novel antisense compound of 8-80 nucleobases

CC in length targeted to, and which specifically hybridizes with, a nucleic

CC acid molecule encoding transforming growth factor (TGF)-beta 2, and

CC inhibits the expression of TGF-beta 2. The invention further relates to:

CC a compound 8-80 nucleobases in length that specifically hybridizes with

CC at least an 8-nucleobase portion of an active site on a nucleic acid

CC molecule encoding TGF-beta 2; a composition comprising the compound and a

CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or

CC tissues by contacting the cells or tissues with the compound so that

CC expression of TGF-beta 2 is inhibited; treating an animal having a

CC disease or condition associated with TGF-beta 2 by administering to the

CC animal a therapeutic or prophylactic amount of the compound so that

CC expression of TGF-beta 2 is inhibited; and screening an antisense

CC compound. The antisense compound has cytostatic, neurotropic,

CC neuroprotective, and immunosuppressive activities. The compound,

CC composition and methods are useful for treating a disease or condition

CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.

CC cancer, a neurodegenerative disorder, or a disease or condition involving

CC hyperactivation of an immune response. This polynucleotide sequence

XX represents an antisense oligonucleotide of the invention.

XX Sequence 20 BP; 6 A; 5 C; 3 G; 6 T; 0 U; 0 Other;

Query Match

Best Local Similarity 90.0%; Score 18; DB 12; Length 20;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTCACCAAAATGGAA 18

DB 3 GCTTTCACCAAAATGGAA 20

RESULT 7

ADI80181/c

ID ADI80181 standard; DNA; 20 BP.

XX AC

XX ADI80181;

XX DT

XX 22-APR-2004 (first entry)

XX DE

XX Human transforming growth factor-beta 2 target DNA region, SEQ ID No 182.

XX KW

XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;

KW cytostatic; neurotropic; neuroprotective; immunosuppressive;

KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;

KW immune; ss; human.

XX OS

XX Homo sapiens.

XX PN

XX US2004006030-A1.

XX PD

XX 08-JAN-2004.

XX PF

XX 02-JUL-2002; 2002US-00189267.

XX PR

XX 02-JUL-2002; 2002US-00189267.

XX PA

XX (ISIS-) ISIS PHARM INC.

XX PI

XX Monia BP, Freier SM, Dobie KW;

XX DR

XX WPI; 2004-081742/08.

XX PT

XX New compounds, particularly antisense oligonucleotides targeted to a

PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a

PT neurodegenerative disorder, or a disease involving hyperactivation of

PT immune response.

XX PS

XX Example 16; SEQ ID NO 182; 135pp; English.

XX CC

XX The invention relates to a novel antisense compound of 8-80 nucleobases

CC in length targeted to, and which specifically hybridizes with, a nucleic

CC acid molecule encoding transforming growth factor (TGF)-beta 2, and

CC inhibits the expression of TGF-beta 2. The invention further relates to:

CC a compound 8-80 nucleobases in length that specifically hybridizes with

CC at least an 8-nucleobase portion of an active site on a nucleic acid

CC molecule encoding TGF-beta 2; a composition comprising the compound and a

CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or

CC tissues by contacting the cells or tissues with the compound so that

CC expression of TGF-beta 2 is inhibited; treating an animal having a

CC disease or condition associated with TGF-beta 2 by administering to the

CC animal a therapeutic or prophylactic amount of the compound so that

CC expression of TGF-beta 2 is inhibited; and screening an antisense

CC compound. The antisense compound has cytostatic, neurotropic,

CC neuroprotective, and immunosuppressive activities. The compound,

CC composition and methods are useful for treating a disease or condition

CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.

CC cancer, a neurodegenerative disorder, or a disease or condition involving

CC hyperactivation of an immune response. This polynucleotide sequence

CC represents a preferred target DNA region of TGF-beta 2 of the invention.

XX Sequence 20 BP; 6 A; 3 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 90.0%; Score 18; DB 12; Length 20;

Best Local Similarity 100.0%; Pred. No. 44;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTACCAAAATGGAA 18
 Db 18 GCTTTACCAAAATGGAA 1

RESULT 8

AAZ65470
 ID AAZ65470 standard; DNA; 16 BP.

XX AC AAZ65470;

XX DT 30-MAR-2000 (first entry)

XX DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-14/3.

XX KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
 KW monocyte chemoattractant protein-1; MCP-1; ulcerative colitis; diabetes;
 KW glomerulonephritis; acute respiratory distress syndrome; ss;
 KW atherosclerosis.

XX OS Unidentified.

XX PN WO9963975-A2.

XX PD 16-DEC-1999.

XX PF 10-JUN-1999; 99WO-EP004013.

XX PR 10-JUN-1998; 98EP-00110709.

XX PR 25-JUL-1998; 98EP-00113974.

XX PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX PI Schlingensiepen K, Schlingensiepen R, Brysch W;

XX DR WPI; 2000-097470/08.

XX PT Composition containing immune stimulant and inhibitor of agent that
 PT adversely affects the immune response, for treating cancers and
 PT infections.

XX PS Claim 5; Fig 1; 30pp; English.

XX CC This sequence is an immunosuppressant inhibitor oligonucleotide, which is
 CC used in the invention. The invention relates to a composition which
 CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.
 CC transforming growth factor TGF-beta, vascular endothelial growth factor
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
 CC that adversely affects the immune response. The composition also includes
 CC at least one stimulant that positively affects the immune response. This
 CC oligonucleotide is an example of an inhibitor that is used in the
 CC composition. The composition is used as an immunostimulant for the
 CC treatment of neoplasms and infections, particularly hyperproliferation;
 CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
 CC most of which are directed against TGFbeta or VEGF, are inhibitors of
 CC monocyte chemoattractant protein-1 (MCP-1) and are useful as anti-
 CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress
 CC syndrome and the formation of atherosclerotic plaque

XX SQ Sequence 16 BP; 6 A; 4 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 3; Length 16;

Best Local Similarity 100.0%; Pred. No. 4.4e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCACCAAAATTCGAAGC 20
 Db 1 TCACCAAAATTCGAAGC 16

RESULT 9

AAQ78430
 ID AAQ78430 standard; DNA; 18 BP.

XX AC AAQ78430;

XX DT 25-MAR-2003 (revised)

XX DT 27-JUN-1995 (first entry)

XX DE TGF-beta gene phosphorothioate antisense oligonucleotide.

XX KW Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;
 KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;
 KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;
 KW immunosuppression; oligonucleotide; ss.

XX OS Synthetic.

XX PN WO9425588-A2.

XX PD 10-NOV-1994.

XX PF 29-APR-1994; 94WO-EP001362.

XX PR 30-APR-1993; 93EP-00107089.

XX PR 13-MAY-1993; 93EP-00107849.

XX PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX PI Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;

XX PI Bogdahn U;

XX DR WPI; 1994-358266/44.

XX PT New transforming growth factor beta anti-sense oligonucleotide(s) - for
 PT treating immunosuppression, tumours, etc.

XX PS Claim 6; Page 46; 74pp; English.

XX CC The antisense oligonucleotides are useful in the treatment of tumours in
 CC which expression of TGF-beta is of relevance for pathogenicity and/or
 CC inhibition of pathological angiogenesis. They are used especially for the
 CC treatment of the immunosuppressive effect of TGF-beta, augmentation of
 CC the proliferation of cytotoxic lymphocytes, treatment of endogenous
 CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas
 CC and malignant gliomas, including glioblastomas, treatment and prophylaxis
 CC of skin carcinogenesis, and treatment of oesophageal and gastric
 CC carcinomas. See AAQ78352-078488. The sequences given in GENESQ files
 CC AAQ78352-078407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-
 CC beta 1. The sequences given in GENESQ files AAQ78408-78487 are antisense
 CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
 CC analogues. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 18 BP; 7 A; 4 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 4.4e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCACCAAAATTCGAAGC 20
 Db 1 TCACCAAAATTCGAAGC 16

RESULT 10

AAZ65453

ID AAZ65453 standard; DNA; 18 BP.

XX

AC AA265453;
 XX
 DT 30-MAR-2000 (first entry)
 XX
 DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-13.
 XX
 KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
 KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;
 KW glomerulonephritis; acute respiratory distress syndrome; ss;
 KW atherosclerosis.
 XX
 OS Unidentified.
 XX
 XX WO9963975-A2.
 PN
 XX
 PD 16-DEC-1999.
 XX
 XX 10-JUN-1999; 99WO-EP004013.
 XX
 XX 10-JUN-1998; 98EP-00110709.
 PR
 PR 25-JUL-1998; 98EP-00113974.
 XX
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 XX
 XX Schlingensiepen K, Schlingensiepen R, Brysch W;
 PI
 XX
 DR WPI; 2000-097470/08.
 XX
 XX Composition containing immune stimulant and inhibitor of agent that
 PT adversely affects the immune response, for treating cancers and
 PT infections.
 XX
 XX Claim 5; Fig 1; 30pp; English.
 XX
 CC This sequence is an immunosuppressant inhibitor oligonucleotide, which is
 CC used in the invention. The invention relates to a composition which
 CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.
 CC transforming growth factor TGF-beta, vascular endothelial growth factor
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
 CC that adversely affects the immune response. The composition also includes
 CC at least one stimulant that positively affects the immune response. This
 CC oligonucleotide is an example of an inhibitor that is used in the
 CC composition. The composition is used as an immunostimulant for the
 CC treatment of neoplasms and infections, particularly hyperproliferation;
 CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
 CC most of which are directed against TGFbeta or VEGF, are inhibitors of
 CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
 CC inflammatories for treating e.g. asthma, Crohn's disease, ulcerative
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress
 CC syndrome and the formation of atherosclerotic plaque
 XX
 SQ Sequence 18 BP; 7 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
 Query Match 80.0%; Score 16; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 TCACCAAAATTGGAAGC 20
 Db 1 TCACCAAAATTGGAAGC 16
 RESULT 11
 AEB01190
 ID AEB01190 standard; DNA; 18 BP.
 XX
 AC AEB01190;
 XX

DT 08-SEP-2005 (first entry)
 XX
 DE TGF-beta 2 inhibition oligonucleotide SEQ ID NO 34.
 XX
 KW pharmaceutical; cell death; neoplasm; ss; Cytostatic; Apoptotic;
 KW immunostimulant; Antiarthritic; Antirheumatic; Antipsoriatic;
 KW TGF-beta antagonist; Vaccine.
 XX
 OS Synthetic.
 PN WO2005059133-A2.
 XX
 XX 30-JUN-2005.
 XX
 XX 20-DEC-2004; 2004WO-EP053604.
 PF
 XX 19-DEC-2003; 2003EP-00029367.
 PR
 PR 05-FEB-2004; 2004US-0541771P.
 XX
 XX (ANTI-) ANTISENSE PHARMA GMBH.
 PA
 XX Schlingensiepen K, Schlingensiepen R;
 PI
 XX WPI; 2005-479334/48.
 DR
 XX Pharmaceutical composition useful for treating neoplasm, comprises
 PT stimulators stimulating function of immune system and/or immune cells and
 PT substances inhibiting cell proliferation and/or inducing cell death.
 XX
 XX Claim 4; SEQ ID NO 34; 46pp; English.
 XX
 CC The invention relates to a pharmaceutical composition (PC) comprising one
 CC or more stimulators that stimulate the function of immune system and/or
 CC immune cells and one or more substances inhibiting cell proliferation
 CC and/or inducing cell death. A pharmaceutical composition is useful for
 CC treating neoplasms chosen from solid tumors; blood born tumors such as
 CC leukemias, acute or chronic myelotic or lymphoblastic leukemia; tumor
 CC metastasis; benign tumors; or is chosen from bile duct carcinoma, bladder
 CC carcinoma, brain tumor, breast carcinoma, bronchogenic carcinoma,
 CC carcinoma of kidney, choriocarcinoma, cystadenocarcinoma, embryonal
 CC carcinoma, epithelial carcinoma, esophageal carcinoma, cervical
 CC carcinoma, colon carcinoma, colorectal carcinoma, endometrial carcinoma,
 CC gallbladder carcinoma, gastric carcinoma, head and neck carcinoma, liver
 CC carcinoma, lung carcinoma, medullary carcinoma, non-small cell
 CC bronchogenic/lung carcinoma, ovarian carcinoma, pancreas carcinoma,
 CC papillary carcinoma, papillary adenocarcinoma, prostate carcinoma, small
 CC intestine carcinoma, rectal carcinoma, renal cell carcinoma, skin
 CC carcinoma, small-cell bronchogenic/lung carcinoma, squamous cell
 CC carcinoma, sebaceous gland carcinoma, testicular carcinoma, uterine
 CC carcinoma, rheumatoid arthritis and psoriasis. The present sequence
 CC represents a TGF-beta 2 inhibition oligonucleotide.
 XX
 SQ Sequence 18 BP; 7 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
 Query Match 80.0%; Score 16; DB 14; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 TCACCAAAATTGGAAGC 20
 Db 1 TCACCAAAATTGGAAGC 16
 RESULT 12
 AA265469
 ID AA265469 standard; DNA; 15 BP.
 XX
 AC AA265469;
 XX
 DT 30-MAR-2000 (first entry)
 XX
 DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-14/2.
 XX

KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
 KW monocyte chemoattractant protein-1; MCP-1; ulcerative colitis; diabetes;
 KW glomerulonephritis; acute respiratory distress syndrome; ss;
 KW atherosclerosis.

XX Unidentified.

XX WO9963975-A2.

XX 16-DEC-1999.

XX 10-JUN-1999; 99WO-EP040413.

XX 10-JUN-1998; 98EP-00110709.

XX 25-JUL-1998; 98EP-00113974.

XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX Schlingensiepen K, Schlingensiepen R, Brysch W;

XX WPI; 2000-097470/08.

XX Composition containing immune stimulant and inhibitor of agent that
 PT adversely affects the immune response, for treating cancers and
 PT infections.

XX Claim 5; Fig 1; 30pp; English.

XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is
 CC used in the invention. The invention relates to a composition which
 CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.
 CC transforming growth factor TGF-beta, vascular endothelial growth factor
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
 CC that adversely affects the immune response. The composition also includes
 CC at least one stimulant that positively affects the immune response. This
 CC oligonucleotide is an example of an inhibitor that is used in the
 CC composition. The composition is used as an immunostimulant for the
 CC treatment of neoplasms and infections, particularly hyperproliferation;
 CC leukaemia; (non-Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
 CC most of which are directed against TGFbeta or VEGF, are inhibitors of
 CC monocyte chemoattractant protein-1 (MCP-1) and are useful as anti-
 CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress
 CC syndrome and the formation of atherosclerotic plaque

XX Sequence 15 BP; 6 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 75.0%; Score 15; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 CACCAAAATTTGGAAGC 20

Db 1 CACCAAAATTTGGAAGC 15

RESULT 13

AAD48552/c

ID AAD48552 standard; DNA; 20 BP.

XX AAD48552;

XX 24-FEB-2003 (first entry)

XX Chicken lysozyme gene fragment sequencing PCR primer, lys056for.

XX Lysozyme gene expression control region; chromosomal positional effect;
 KW transgene; avian cell; PCR; primer; chicken; ss.

XX OS

Gallus sp.

XX WO200279447-A2.

XX 10-OCT-2002.

XX 29-MAR-2002; 2002WO-US009866.

XX 30-MAR-2001; 2001US-0280004P.

XX 03-AUG-2001; 2001US-00922549.

XX 25-JAN-2002; 2002US-0351550P.

XX (AVIG-) AVIGENICS INC.

XX Rapp JC;

XX WPI; 2003-046807/04.

XX New isolated or recombinant nucleic acid for reducing the chromosomal
 PT positional effect of a transgene, comprises an isolated avian lysozyme
 PT gene expression control region.

XX Example 1; Fig 1; 89pp; English.

XX The invention relates to an isolated or recombinant nucleic acid or DNA
 CC molecule comprising an isolated avian lysozyme gene expression control
 CC region operably linked to a nucleic acid insert encoding a polypeptide.
 CC The nucleic acid is useful for reducing the chromosomal positional effect
 CC of a transgene operably linked to the lysozyme gene expression control
 CC region and transfected into a recipient avian cell. The present sequence
 CC is a PCR primer used for sequencing chicken lysozyme gene expression
 CC control region

XX Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 8; Length 20;

Best Local Similarity 84.2%; Pred. No. 3.6e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GCTTTTCCCAAAATTTGGAAG 19

Db 20 GCTGTCCCAACATGGAAG 2

RESULT 14

ADK78448/c

ID ADK78448 standard; DNA; 20 BP.

XX ADK78448;

XX 20-MAY-2004 (first entry)

XX Chimeric phosphorothioate oligonucleotide to target Nav1.3 #5782.

XX Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;

XX diabetic neuropathy; arthritic pain; migraine headache;

XX infantile epilepsy; ataxia; ss.

XX Synthetic.

XX WO2004016754-A2.

XX 26-FEB-2004.

XX 14-AUG-2003; 2003WO-US025465.

XX 14-AUG-2002; 2002US-0403416P.

XX (PHAA) PHARMACIA CORP.

XX Roberds SL;

XX

DR WPI; 2004-203785/19.
XX New antisense compound targeted to a nucleic acid molecule encoding
PT Navi1.3, useful for treating a disease or condition associated
PT with Navi1.3, e.g. pain, seizure disorder such as childhood seizure
PT disorder, or ataxia.
XX
PS Claim 4; SEQ ID NO 5782; 417pp; English.
XX
CC The present invention relates to an antisense compound targeted to a
CC nucleic acid molecule encoding Navi1.3, where the antisense compound
CC specifically hybridizes with and inhibits the expression of Navi1.3. The
CC compound and composition are useful for treating a disease or condition
CC associated with Navi1.3, e.g. pain including but not limited to
CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC pain from burns, migraine headache, cluster headache, mild-to-moderate
CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
CC sequence represents a chimeric phosphorothioate oligonucleotide with
CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of
CC human Navi1.3 expression, the oligonucleotides are designed to target
CC different regions of the human Navi1.3 RNA.
XX
SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 71.0%; Score 14.2; DB 12; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GCTTTCACCAAAATGGGAAG 19
DB 19 GCTTCCAGCAATGGGAAG 1
RESULT 15
ADK78529/c
ID ADK78529 standard; DNA; 20 BP.
XX
AC ADK78529;
XX
DT 20-MAY-2004 (first entry)
XX
DE Chimeric phosphorothioate oligonucleotide to target Navi1.3 #5863.
XX
KW Navi1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
KW diabetic neuropathy; arthritic pain; migraine headache;
KW infantile epilepsy; ataxia; ss.
XX
OS Synthetic.
XX
PN WO2004016754-A2.
XX
PD 26-FEB-2004.
XX
PF 14-AUG-2003; 2003WO-US025465.
XX
PR 14-AUG-2002; 2002US-0403416P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Roberts SL;
XX
DR WPI; 2004-203785/19.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT Navi1.3, useful for treating a disease or condition associated
PT with Navi1.3, e.g. pain, seizure disorder such as childhood seizure
PT disorder, or ataxia.
XX
PS Claim 4; SEQ ID NO 5863; 417pp; English.
XX
CC The present invention relates to an antisense compound targeted to a

nucleic acid molecule encoding Navi1.3, where the antisense compound
specifically hybridizes with and inhibits the expression of Navi1.3. The
compound and composition are useful for treating a disease or condition
associated with Navi1.3, e.g. pain including but not limited to
neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
pain from burns, migraine headache, cluster headache, mild-to-moderate
but not limited to neonatal or infantile epilepsy; or ataxia. The present
sequence represents a chimeric phosphorothioate oligonucleotide with
2'MOE wings and a deoxy gap. Used during the antisense inhibition of
human Navi1.3 expression, the oligonucleotides are designed to target
different regions of the human Navi1.3 RNA.
SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 71.0%; Score 14.2; DB 12; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GCTTTCACCAAAATGGGAAG 19
DB 20 GCTTCCAGCAATGGGAAG 2
Search completed: March 4, 2006, 02:31:42
Job time : 393.947 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 4, 2006, 01:46:27 ; Search time 3170.53 Seconds
(without alignments)
295.138 Million cell updates/sec

Title: US-09-701-583A-14

Perfect score: 20

Sequence: 1 gcttcacaaattggaagc 20

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 106998

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_hc:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_gss1:*

10: gb_gss2:*

11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	13.4	67.0	34	1	AV852639
C 2	12.8	64.0	25	10	CG729682
C 3	12.8	64.0	31	1	AI034270
C 4	12.6	63.0	33	9	BZ769257
5	12.4	62.0	35	9	AZ336391
6	12.2	61.0	26	9	BH863411
7	12.2	61.0	34	9	AZ645914
C 8	12	60.0	21	9	AZ308115
C 9	12	60.0	27	10	AG204809
C 10	12	60.0	32	9	BH904979
C 11	12	60.0	32	10	AJ600156
C 12	11.8	59.0	31	1	AU255583
C 13	11.8	59.0	32	5	BQ587054
C 14	11.8	59.0	36	9	BZ661352
15	11.8	59.0	37	1	AI823627
16	11.8	59.0	40	1	AA887375
17	11.8	59.0	40	1	AA961031
18	11.6	58.0	31	11	CR395105
19	11.6	58.0	34	9	AZ789746
C 20	11.6	58.0	34	11	CR358544
C 21	11.6	58.0	35	9	BH854633
22	11.4	57.0	19	1	AI790036

C 23	11.4	57.0	31	9	BH792339
24	11.4	57.0	34	9	BH905278
25	11.4	57.0	36	10	CZ469111
26	11.2	56.0	28	11	TA285H02Q
C 27	11.2	56.0	29	9	CC794724
C 28	11.2	56.0	32	9	AZ309847
29	11.2	56.0	33	11	DR23D20T
30	11.2	56.0	34	6	CF302443
C 31	11.2	56.0	34	9	AZ761083
C 32	11.2	56.0	34	9	AZ781725
C 33	11.2	56.0	36	9	AZ864054
C 34	11.2	56.0	36	10	CL528503
C 35	11.2	56.0	37	9	BH811021
C 36	11.2	56.0	37	9	BH865074
C 37	11.2	56.0	37	9	BH903531
C 38	11.2	56.0	38	1	AU259281
C 39	11.2	56.0	39	9	BH856768
C 40	11	55.0	21	10	AJ596091
41	11	55.0	28	10	CZ469769
42	11	55.0	28	10	CZ471273
C 43	11	55.0	29	9	AZ580321
44	11	55.0	34	9	AZ658401
C 45	11	55.0	35	10	CZ471370

ALIGNMENTS

RESULT 1
AV852639/c 34 bp mRNA linear EST 08-NOV-2001
LOCUS AV852639 Nori Satoh unpublished cDNA library, larva Ciona
DEFINITION intestinalis cDNA clone rcilv19c08 3', mRNA sequence.
ACCESSION AV852639
VERSION AV852639.1 GI:16837973
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
REFERENCE 1 (bases 1 to 34)
AUTHORS Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
TITILE Expressed genes in Ciona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES

Location/Qualifiers
1..34
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="rcilv19c08"
/tissue_type="whole animal"
/dev_stages="larva"
/clone_lib="Nori Satoh unpublished cDNA library, larva"

ORIGIN

Query Match 67.0%; Score 13.4; DB 1; Length 34;
Best Local Similarity 93.3%; Pred.No. 8e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 4 TTCACCAAAATGGAA 18
|||||
Db 32 TTCACCAAAATGGAA 18

RESULT 2
CG729682/c

```

LOCUS      CG729682      25 bp      DNA      linear      GSS 20-OCT-2003
DEFINITION 1119114B03 2EL_y1 1119 - RescueMu Grid AA Zea mays genomic, genomic
survey sequence.
ACCESSION  CG729682
VERSION     CG729682.1  GI:37771623
KEYWORDS   GSS.
SOURCE     Zea mays
ORGANISM   Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 25)
AUTHORS    Walbot V.
TITLE      Maize genomic sequences found using engineered RescueMu transposon
JOURNAL    Unpublished (2001)
COMMENT    Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Possible ligation site of ends cut by 2 different endonucleases.
            Reverse complemented post-ligation sequence from source sequence.
            Plate: 1119114 row: B column: 03
            Class: transposon-tagged.
FEATURES   source
            1..25
            /organism="Zea mays"
            /mol_type="genomic DNA"
            /cultivar="mixed background W23/A188/B73/K55"
            /db_xref="taxon:4577"
            /tissue_type="leaf"
            /dev_stage="adult"
            /lab_host="DH10B"
            /clone_lib="1119 - RescueMu Grid AA"
            /note="Organ: leaf; Vector: RescueMu (engineered from
            pBluescript backbone); Site 1: BamHI; Site 2: BglII;
            RescueMu is a 4.9 kb, modified maize Mu transposon
            designed to allow plasmid rescue from total genomic DNA.
            Mu elements insert preferentially into transcription
            units. For more information on RescueMu, go to the web
            site 'www.zmndb.iastate.edu' and follow the links for
            'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
            was extracted from leaf strips, double digested using
            BamHI and BglII, and ligated to form circular plasmids.
            DH10B cells were transformed and then screened on LB
            plates with ampicillin."
ORIGIN
Query Match      64.0%; Score 12.8; DB 10; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.5e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3  TTTTCCACCAAAATGGAA 18
        ||| ||||| |||||
Db       25  TTTTCCACCAAAATGGAA 10

RESULT 3
AI034270/c
LOCUS      AI034270      31 bp      mRNA      linear      EST 25-JUN-1998
DEFINITION OW15H03.x1 Soares parathyroid tumor_NDHPA Homo sapiens cDNA clone
IMAGE:1646933 3' similar to TR:P97536 P97536 TIP120.1; mRNA
sequence.
ACCESSION  AI034270
VERSION     AI034270.1  GI:3255223
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.

LOCUS      BZ769257      33 bp      DNA      linear      GSS 13-MAR-2003
DEFINITION SALK_141859.37.05.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_141859.37.05.x, genomic
survey sequence.
ACCESSION  BZ769257
VERSION     BZ769257.1  GI:28942941
KEYWORDS   GSS.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
            1 (bases 1 to 33)
REFERENCE  Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
            A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome

```

```

REFERENCE  1 (bases 1 to 31)
AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL    Unpublished (1997)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: gcgaps-r@mail.nih.gov
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Seq primer: -40m3 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES   Location/Qualifiers
            1..31
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:1646933"
            /tissue_type="parathyroid tumor"
            /dev_stage="adult"
            /lab_host="DH10B (ampicillin resistant)"
            /clone_lib="Soares parathyroid tumor_NDHPA"
            /note="Organ: parathyroid gland; Vector: pT7T3D
            (Pharmacia) with a modified polylinker; Site 1: Not I;
            Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
            oligo(dT) primer
            [5'-TGTTACCAATCTGAAGTGGGCGCGCCACCAATTTTCTTTTCTTTTCTTTT
            TTTT-3'], double-stranded cDNA was size selected, ligated
            to Eco RI adapters (Pharmacia), digested with Not I and
            cloned into the Not I and Eco RI sites of a modified pT7T3
            vector (Pharmacia). Library went through one round of
            normalization to a Cot = 5. Library constructed by Bento
            Soares and M. Fatima Bonaldo. RNA from sporadic parathyroid
            adenomas was kindly provided by Dr. Stephen Marx, National
            Institute of Diabetes and Digestive and Kidney Diseases,
            NIH."
ORIGIN
Query Match      64.0%; Score 12.8; DB 1; Length 31;
Best Local Similarity 87.5%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3  TTTTCCACCAAAATGGAA 18
        ||| ||||| |||||
Db       19  TTTCCAGCAAAATGGAA 4

RESULT 4
BZ769257/c
LOCUS      BZ769257/c
DEFINITION Arabidopsis thaliana genomic clone SALK_141859.37.05.x, genomic
survey sequence.
ACCESSION  BZ769257
VERSION     BZ769257.1  GI:28942941
KEYWORDS   GSS.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
            1 (bases 1 to 33)
REFERENCE  Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
            A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome

```

JOURNAL
COMMENT

Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At5g35820.
Class: TDNA tagged.

FEATURES

Location/Qualifiers
1..33

/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK 141859.37.05.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 63.0%; Score 12.6; DB 9; Length 33;
Best Local Similarity 78.9%; Pred. No. 2e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCTTCCACCAAAATGGAAG 19
||||| ||| ||| |||
DB 32 GCTTTCAGCAAGTTGTAG 14

RESULT 5
A2336391

LOCUS 35 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0066G07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0066G07 R, genomic survey sequence.

ACCESSION A2336391
VERSION A2336391.1 GI:10405642

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0066 row: G column: 07
Seq primer: CACACGAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 35.

FEATURES

Location/Qualifiers
1..35
/organism="Mus musculus"

source

/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0066G07"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. Coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 62.0%; Score 12.4; DB 9; Length 35;
Best Local Similarity 92.9%; Pred. No. 2.6e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTTTCACCAAAATG 15
||||| ||| ||| |||
DB 1 CTATCACCAAAATG 14

RESULT 6

BH863411

LOCUS

DEFINITION BH863411 26 bp DNA linear GSS 05-AUG-2002
SALK_093836 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_093836, genomic survey sequence.

ACCESSION BH863411
VERSION BH863411.1 GI:22099002

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (chale cress)

ORGANISM

Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE

AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J., and Ecker, J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome

JOURNAL

COMMENT Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers
1..26
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"

FEATURES

source
Location/Qualifiers
1..26
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"

/clone="SALK 093836"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 61.0%; Score 12.2; DB 9; Length 26;
 Best Local Similarity 82.4%; Pred. No. 3.1e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TTACCAAAATTTGAAGC 20
 |||||
 Db 9 TACAGCAATTTGAAGC 25

RESULT 7

AZ645914
 LOCUS 34 bp DNA linear GSS 14-DEC-2000
 DEFINITION IM0511K08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0511K08 R, genomic survey sequence.

ACCESSION AZ645914
 VERSION
 KEYWORDS
 SOURCE

ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0511 row: K column: 08

Seq primer: CACACAGGAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 34.

FEATURES

Location/Qualifiers

1..34

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0511K08"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 61.0%; Score 12.2; DB 9; Length 34;
 Best Local Similarity 82.4%; Pred. No. 3.2e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CTTTCACCAAAATTTGGAA 18
 |||||
 Db 2 CTTTCACCAAAATTTGGAA 18

RESULT 8

AZ308115/c

LOCUS

DEFINITION 21 bp DNA linear GSS 29-SEP-2000
 clone UUGC1M0010J17 R, genomic survey sequence.

ACCESSION AZ308115

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0010 row: J column: 17

Seq primer: CACACAGGAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

FEATURES

Location/Qualifiers

1..21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0010J17"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number-inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 60.0%; Score 12; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTTCACCAAT 13
|||||
DB 20 GTTTCACCAAT 9

RESULT 9

AG204809/c

LOCUS

DEFINITION Pan troglodytes DNA, clone: RP43-090L01.T7, genomic survey sequence.

ACCESSION

AG204809

VERSION

AG204809.1 GI:45236984

KEYWORDS

GSS.

SOURCE

Pan troglodytes (chimpanzee)

ORGANISM

Pan troglodytes

REFERENCE

1

AUTHORS

Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.

TITLE

BAC end sequences of Library RP-43

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 27)

AUTHORS

Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.

TITLE

Direct Submission

JOURNAL

Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC); 52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea

REFERENCE

(E-mail: redstone@mail.krribb.re.kr URL: http://phs.grc.krribb.re.kr/, Tel: 82-42-866-7181, Fax: 82-42-860-4409)

COMMENT

Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

PRIMERS

Sequencing: T7

LIBRARY

Vector : pBACe3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI.

FEATURES

Location/Qualifiers

1..27

/organism="Pan troglodytes"

/mol_type="genomic DNA"

/db_xref="taxon:9598"

/clone="RP43-090L01.T7"

/sex="male"

/cell_type="lymphocytes"

/clone_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match

Best Local Similarity

Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCTTTCACCAATTTGGAAGC 20

|||||

DB 31 GCTTTCACCAATTTGGAAGC 12

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QY 1 GCTTTCACCAATTTGGAAGC 20

|||||

DB 31 GCTTTCACCAATTTGGAAGC 12

|||||

QY 1 GCTTTCACCAATTTGGAAGC 20

|||||

DB 31 GCTTTCACCAATTTGGAAGC 12

|||||

QY 1 GCTTTCACCAATTTGGAAGC 20

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DB 31 GCTTTCACCAATTTGGAAGC 12

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QY 1 GCTTTCACCAATTTGGAAGC 20

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DB 31 GCTTTCACCAATTTGGAAGC 12

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QY 1 GCTTTCACCAATTTGGAAGC 20

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DB 31 GCTTTCACCAATTTGGAAGC 12

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QY 1 GCTTTCACCAATTTGGAAGC 20

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DB 31 GCTTTCACCAATTTGGAAGC 12

|||||

QY 1

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REFERENCE
AUTHORS      Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,
              Chauvin, S., Bechold, N., Cruaud, C., Derose, R., Pelletier, G.,
              Lepiniec, L., Caboche, M. and Lecharny, A.
TITLE        T-DNA integration into the Arabidopsis genome depends on sequences
              of pre-insertion sites
JOURNAL      EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED       12446585
LOCUS        2 (bases 1 to 32)
REFERENCE    Balzerque, S.
AUTHORS      Direct Submission
TITLE        Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
              Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT      PCR was performed on DNA from transformants of Arabidopsis thaliana
              plants from INRA (Versailles). The DNA fragment(s) resulting from
              the PCR were directly sequenced from the left or the right border
              to determine the genomic sequence flanking the insertion. T-DNA
              derived sequences were removed. Information to order the
              corresponding mutant line and a link to a database providing a
              graphical display of the insertion site are available at
              http://dbgap.versailles.inra.fr/publiclines/. This sequence has
              been generated in the framework of the French plant genomics
              program 'Genoplante' (http://www.genoplante.com and
              http://genoplante-info.infobiogen.fr).
FEATURES     Location/Qualifiers
              1..32
              /organism="Arabidopsis thaliana"
              /mol_type="genomic DNA"
              /db_xref="taxon:3702"
              /clone="501C03"
              /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
              /ecotype="Wassilewskija"
misc_feature  1..32
              /note="T-DNA flanking sequence
              right border"
ORIGIN
Query Match      60.0%; Score 12; DB 10; Length 32;
Best Local Similarity 75.0%; Pred. NO. 4e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  1  GCTTTCACCAAAATTTGGAAGC 20
    ||||| ||||| |||||
Db   1  GCTTTCCTCCACTGTGGAGC 20

RESULT 12
AU255583/c
LOCUS        31 bp mRNA linear EST 25-APR-2002
DEFINITION   AU255583 3'-directed mouse cDNA library Mus musculus cDNA clone
              BED0005815 3', mRNA sequence.
ACCESSION    AU255583
VERSION      AU255583.1 GI:20318461
KEYWORDS     EST.
SOURCE       Mus musculus (house mouse)
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
              Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE    Kato, K. and Matoba, R.
AUTHORS      Graduate School of Biological Sciences
              Nara Institute of Science and Technology
              916-5 Takayama, Ikoma, Nara 630-0101, Japan
JOURNAL      Tel: 81-743-72-5581
              Fax: 81-743-72-5589
              Email: kkatob@bs.nara.ac.jp,
              URL: http://love2.aist-nara.ac.jp/BED/index.html.
              Location/Qualifiers

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              1..31
              /organism="Mus musculus"
              /mol_type="mRNA"
              /db_xref="taxon:10090"
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              /tissue_type="brain"
              /clone_lib="3'-directed mouse cDNA library"
ORIGIN
Query Match      59.0%; Score 11.8; DB 1; Length 31;
Best Local Similarity 86.7%; Pred. NO. 5e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  3  TTTCACCAAAATTTGGA 17
    ||||| ||||| |||||
Db   17 TTTCGCTAAATTTGGA 3

RESULT 13
BO587054/c
LOCUS        BO587054
DEFINITION   BO587054 024-011-H11-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
              024-011-H11 5-PRIME, mRNA sequence.
ACCESSION    BO587054
VERSION      BO587054.1 GI:26116636
KEYWORDS     EST.
SOURCE       Beta vulgaris
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
              Caryophyllales; Amaranthaceae; Beta.
REFERENCE    1 (bases 1 to 32)
AUTHORS      Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,
              Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
              and Radelof, U.
TITLE        Construction of a 'unigene' cDNA clone set by oligonucleotide
              fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL      Plant J. 32 (5), 845-857 (2002)
PUBMED       12472698
COMMENT      Contact: Weishaar B
              ADIS DNA core facility at MPIZ
              Max-Planck-Institute for Plant Breeding Research
              Carl-von-Linne Weg 10, 50829 Koeln, Germany
              Fax: 00492215062851
              Email: weishaar@mpiz-koeln.mpg.de
              Insert Length: 32 Std Error: 0.00
              Plate: 11 row: H column: 11
              Seq primer: SP6; CATACGATTAGGTGACACTATAG.
              Location/Qualifiers
              1..32
              /organism="Beta vulgaris"
              /mol_type="mRNA"
              /cultivar="KWS2320 (double haploid, monogerm breeding
              line)"
              /db_xref="GABI:185812"
              /db_xref="taxon:161934"
              /clone="024-011-H11"
              /tissue_type="leaf"
              /lab_host="EMDH10B"
              /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
              cDNA library from sugar beet. Library provided by KWS
              Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
              b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
              orientation:
              SP6-Sali-CCACGGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
              Sequencing granted in the context of the GABI-Beet
              Project, local PI: Dr. Katharina Schneider, coordinator:
              Prof. Christian Jung; Sequence submission managed by
              RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN
Query Match      59.0%; Score 11.8; DB 5; Length 32;

```

Best Local Similarity 86.7%; Pred. No. 5.1e+05; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTTTCACCAAAATTGG 16

Db 23 CTTTCACCTATATGG 9

RESULT 14

BZ661352

LOCUS

DEFINITION

Arabidopsis thaliana genomic clone SALK_024821.36.20.x, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BZ661352.1 GI:28174499
36 bp DNA linear GSS 31-JAN-2003
SALK_024821.36.20.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_024821.36.20.x, genomic survey sequence.

REFERENCE

AUTHORS

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmermann, J. and Ecker, J.R.

TITLE

A Sequence-Indexed Library of Insertion Mutations in the

JOURNAL

COMMENT

Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At2g17360.

Class: TDNA tagged.

FEATURES

source

1..36

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_024821.36.20.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 59.0%; Score 11.8; DB 9; Length 36;
Best Local Similarity 86.7%; Pred. No. 5.1e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TTTTCACCAAAATTGGA 17

Db 1 TCTGACCAAAATTGGA 15

RESULT 15

A1823627

LOCUS

DEFINITION

A1823627
w185e02.x1 NCI CGAP Kid12 Homo sapiens cDNA clone IMAGE:2400122 3, similar to SW.GB13 HUMAN Q14344 GUANINE NUCLEOTIDE-BINDING PROTEIN, ALPHA-13 SUBUNIT. ?; mRNA sequence.

ACCESSION

VERSION

KEYWORDS

EST.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

EMAIL

TISSUE

EMMERIT-BUCK, M.D., Ph.D.

CDNA LIBRARY PREPARATION: M. Bento Soares, Ph.D.

DNA SEQUENCING BY: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 1024 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1..37

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2400122"

/tissue type="2 pooled tumors (clear cell type)"

/lab host="DH10B"

/clone lib="NCI CGAP Kid12"

/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI;

Plasmid DNA from the normalized library NCI-CGAP Kids was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1323912-1325831, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match

Best Local Similarity

Matches 13; Conservative

0; Mismatches 2; Indels

0; Gaps

QY

Db

Search completed: March 4, 2006, 03:38:57

Job time : 3174.53 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 4, 2006, 01:49:32 ; Search time 76.8421 Seconds
(without alignments)
462.653 Million cell updates/sec

Title: US-09-701-583A-14

Perfect score: 20

Sequence: 1 gcttcacaaattggaagc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1198766

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/prodata/1/ina/1 COMB.seq.*
2: /cgn2_6/prodata/1/ina/5 COMB.seq.*
3: /cgn2_6/prodata/1/ina/6A COMB.seq.*
4: /cgn2_6/prodata/1/ina/68 COMB.seq.*
5: /cgn2_6/prodata/1/ina/H COMB.seq.*
6: /cgn2_6/prodata/1/ina/PCTUS COMB.seq.*
7: /cgn2_6/prodata/1/ina/PP COMB.seq.*
8: /cgn2_6/prodata/1/ina/RE COMB.seq.*
9: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	80.0	18	3	US-08-535-249-79
2	14.2	71.0	25	3	US-09-396-196G-6827
3	13.8	69.0	29	3	US-09-304-232-470
4	13.2	66.0	24	2	US-08-465-590-42
5	13.2	66.0	24	3	US-08-711-417C-42
6	13.2	66.0	24	3	US-09-723-909-42
7	13.2	66.0	24	6	PCR-US93-08743-42
8	13.2	66.0	25	3	US-09-396-196G-122784
9	12.8	64.0	19	3	US-09-696-791-4062
10	12.8	64.0	19	3	US-09-696-791-4063
11	12.8	64.0	25	3	US-09-396-196G-71637
12	12.8	64.0	25	3	US-09-396-196G-71638
13	12.8	64.0	25	3	US-09-396-196G-71639
14	12.8	64.0	25	3	US-09-396-196G-71640
15	12.8	64.0	25	3	US-09-396-196G-71641
16	12.8	64.0	25	3	US-09-396-196G-71642
17	12.8	64.0	26	2	US-08-118-387-4
18	12.8	64.0	29	2	US-08-306-871-39
19	12.8	64.0	29	2	US-08-569-959-39
20	12.8	64.0	30	3	US-08-544-381B-137
21	12.6	63.0	21	2	US-08-814-806-12
22	12.6	63.0	21	3	US-09-293-854-12
23	12.6	63.0	25	3	US-09-396-196G-16724
24	12.6	63.0	25	3	US-09-396-196G-18361

25	12.6	63.0	25	3	US-09-396-196G-40788
26	12.6	63.0	25	3	US-09-396-196G-62362
27	12.6	63.0	25	3	US-09-396-196G-81441
28	12.6	63.0	25	3	US-09-396-196G-81442
29	12.6	63.0	25	3	US-09-396-196G-81443
30	12.6	63.0	25	3	US-09-396-196G-81444
31	12.6	63.0	27	3	US-09-012-087A-40
32	12.6	63.0	27	3	US-09-481-620A-58
33	12.6	63.0	27	3	US-09-781-804-39
34	12.6	63.0	28	3	US-09-589-483-6
35	12.6	63.0	28	3	US-09-589-777C-6
36	12.6	63.0	30	3	US-08-444-818-196
37	12.6	63.0	38	3	US-09-231-077D-2
38	12.4	62.0	20	3	US-09-629-645A-31
39	12.2	61.0	25	3	US-09-396-196G-9005
40	12.2	61.0	25	3	US-09-396-196G-9647
41	12.2	61.0	25	3	US-09-396-196G-13788
42	12.2	61.0	25	3	US-09-396-196G-13789
43	12.2	61.0	25	3	US-09-396-196G-18088
44	12.2	61.0	25	3	US-09-396-196G-18089
45	12.2	61.0	25	3	US-09-396-196G-127149

ALIGNMENTS

RESULT 1

US-08-535-249-79
; Sequence 79, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown

TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-535-249-79

Query Match 80.0%; Score 16; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TCACCAAAATTTGGAAGC 20
| | | | | | | | | | | | | | | | | |
Db 1 TCACCAAAATTTGGAAGC 16

RESULT 2
US-09-396-196G-6827
; Sequence 6827, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6827
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-6827

Query Match 71.0%; Score 14.2; DB 3; Length 25;
Best Local Similarity 84.2%; Pred. No. 5.6e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CTTTCACCAAAATTTGGAAGC 20
| | | | | | | | | | | | | | | | | |
Db 5 CTTTCAGCAAGTTAGGAGC 23

RESULT 3
US-09-304-232-470/c
; Sequence 470, Application US/09304232
; Patent No. 6525185
; GENERAL INFORMATION:
; APPLICANT: Fan, Jian Bing
; APPLICANT: Chakravarti, Aravinda
; APPLICANT: Halushka, Marc Kenneth
; APPLICANT: Case Western Reserve University School of Medicine
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Polymorphisms Associated With
; TITLE OF INVENTION: Hypertension
; FILE REFERENCE: 018547-034210US
; CURRENT APPLICATION NUMBER: US/09/304,232
; CURRENT FILING DATE: 1999-05-03
; EARLIER APPLICATION NUMBER: US 60/084,641
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 909
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 470
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: GH2BX3 126
US-09-304-232-470

Query Match 69.0%; Score 13.8; DB 3; Length 29;
Best Local Similarity 78.9%; Pred. No. 9.2e+02;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCTTTCACCAAAATTTGGAAG 19
| | | | | | | | | | | | | | | | | |
Db 25 GTTTTCACCCGTTGGAAG 7

RESULT 4
US-08-465-590-42
; Sequence 42, Application US/08465590
; Patent No. 5824770
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 164
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Ascii (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,590
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/238,212
; FILING DATE: 02-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/121,438
; FILING DATE: 14-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/946,233
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,695
; REFERENCE/DOCKET NUMBER: MPG-006C2DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-465-590-42

Query Match 66.0%; Score 13.2; DB 2; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TTTTCACCAAAATTTGGAAGC 20
| | | | | | | | | | | | | | | | | |
Db 5 TTTAACCAATTTGGAAGC 22

RESULT 5
US-08-711-417C-42
; Sequence 42, Application US/08711417C
; Patent No. 6228611
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE

NUMBER OF SEQUENCES: 202
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA: US/08/711,417C
FILING DATE: 05-Sep-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/238,212
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 08/121,438
FILING DATE: 14-SEP-1993
APPLICATION NUMBER: 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis P.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10287/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-08-711-417C-42
Query Match 66.0%; Score 13.2; DB 3; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 TTTCACCAATTGGGAAGC 20
DB 5 TTTAACCAATTGGGAAGC 22
RESULT 6
US-09-723-909-42
Sequence 42, Application US/097233909
Patent No. 6630141
GENERAL INFORMATION:
APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 202
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA: US/09/723,909
FILING DATE: 28-NOV-6630141-2000

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/711,417
FILING DATE: 05-Sep-1996
APPLICATION NUMBER: 08/238,212
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 08/121,438
FILING DATE: 14-SEP-1993
APPLICATION NUMBER: 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis P.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10287/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-723-909-42
Query Match 66.0%; Score 13.2; DB 3; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 TTTCACCAATTGGGAAGC 20
DB 5 TTTAACCAATTGGGAAGC 22
RESULT 7
PCT-US93-08743-42
Sequence 42, Application PC/TUS9308743
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 152
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08743
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 946,233
FILING DATE: 14-SEP-1992
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PCT-US93-08743-42
Query Match 66.0%; Score 13.2; DB 6; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 TTTCACCAATTGGGAAGC 20
DB 5 TTTAACCAATTGGGAAGC 22

```
RESULT 8
US-09-396-196G-122784
; Sequence 122784, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 122784
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-122784

Query Match      66.0%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TTTTACCAAAATTGGAAGC 20
    ||||| |||||
Db 4 TTTTCACTACAATGGAAGC 21

RESULT 9
US-09-696-791-4062/c
; Sequence 4062, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: SKIN AND EYE DISEASES
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4062
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: PCNA HH ribozyme binding site
; US-09-696-791-4062

Query Match      64.0%; Score 12.8; DB 3; Length 19;
Best Local Similarity 87.5%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTTTACCAAAATTGGA 17
    ||||| |||||
Db 19 CTTTAAACAATTTGA 4

RESULT 10
US-09-696-791-4063/c
; Sequence 4063, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: SKIN AND EYE DISEASES
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; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4063
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: PCNA HH ribozyme binding site
; US-09-696-791-4063

Query Match      64.0%; Score 12.8; DB 3; Length 19;
Best Local Similarity 87.5%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTTTACCAAAATTGGA 17
    ||||| |||||
Db 18 CTTTAAACAATTTGA 3

RESULT 11
US-09-396-196G-71637
; Sequence 71637, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71637
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-71637

Query Match      64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTTTACCAAAATTGG 16
    ||||| |||||
Db 10 GCTGTACCAAAATTGG 25

RESULT 12
US-09-396-196G-71638
; Sequence 71638, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71638
; LENGTH: 25
```

; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-71639

Query Match 64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3e+03; 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Gaps 0;

QY 1 GCTTTCACCAAAATTGG 16
||| ||||| |||||
Db 8 GCTGTACCAAAATTGG 23

RESULT 13
US-09-396-196G-71639
; Sequence 71639, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71639
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-71639

Query Match 64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTTTCACCAAAATTGG 16
||| ||||| |||||
Db 7 GCTGTACCAAAATTGG 22

RESULT 14
US-09-396-196G-71640
; Sequence 71640, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71640
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-71640

Query Match 64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTTTCACCAAAATTGG 16

Db 4 GCTGTACCAAAATTGG 19
||| ||||| |||||

RESULT 15
US-09-396-196G-71641
; Sequence 71641, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71641
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-71641

Query Match 64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTTTCACCAAAATTGG 16
||| ||||| |||||
Db 2 GCTGTACCAAAATTGG 17

Search completed: March 4, 2006, 02:07:26
Job time : 77.8421 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 4, 2006, 01:58:42 ; Search time 495.789 Seconds
(without alignments)
88.444 Million cell updates/sec

Title: US-09-701-583A-14

Perfect score: 20

Sequence: 1 gcttcaccaaattggaagc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters: 11581468

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications NA.New.*
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3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
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12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq4.*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	15.2	76.0	25	12	US-11-121-849-447577
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4	15	75.0	25	12	US-11-121-849-634116
5	14.8	74.0	25	12	US-11-121-849-583444
6	14.4	72.0	24	8	US-10-310-914A-323453
7	14.4	72.0	25	12	US-11-121-849-206297
8	14.4	72.0	25	12	US-11-121-849-206298
9	14.4	72.0	25	12	US-11-121-849-206856
10	14.4	72.0	25	12	US-11-121-849-206857
11	14.2	71.0	25	8	US-10-310-914A-1191627
12	14.2	71.0	25	12	US-11-121-849-191
13	14.2	71.0	25	12	US-11-121-849-345854
14	14.2	71.0	25	12	US-11-121-849-673774
15	14.2	71.0	25	12	US-11-121-849-673775
16	14.2	71.0	25	12	US-11-121-849-673776
17	14.2	71.0	25	12	US-11-121-849-673777
18	13.8	69.0	19	10	US-11-101-244-1430638
19	13.8	69.0	19	11	US-11-083-784-1430638
20	13.8	69.0	20	8	US-10-310-914A-791928

c 21	13.8	69.0	23	8	US-10-310-914A-905108
c 22	13.8	69.0	24	12	US-11-137-315A-19
c 23	13.8	69.0	25	12	US-11-121-849-429730
c 24	13.8	69.0	25	12	US-11-121-849-431098
c 25	13.8	69.0	25	12	US-11-121-849-431099
c 26	13.8	69.0	25	12	US-11-121-849-515908
c 27	13.8	69.0	25	12	US-11-121-849-673778
c 28	13.8	69.0	25	12	US-11-121-849-673779
c 29	13.6	68.0	25	12	US-11-136-527-309344
c 30	13.6	68.0	25	12	US-11-136-527-309345
c 31	13.6	68.0	25	12	US-11-136-527-309352
c 32	13.6	68.0	25	12	US-11-136-527-309363
c 33	13.6	68.0	25	12	US-11-136-527-309371
c 34	13.6	68.0	25	12	US-11-136-527-309372
c 35	13.4	67.0	19	10	US-11-101-244-1149636
c 36	13.4	67.0	19	11	US-11-083-784-1149636
c 37	13.4	67.0	23	8	US-10-310-914A-905217
c 38	13.4	67.0	25	12	US-11-121-849-192
c 39	13.4	67.0	25	12	US-11-121-849-118160
c 40	13.4	67.0	25	12	US-11-121-849-206299
c 41	13.4	67.0	25	12	US-11-121-849-206858
c 42	13.4	67.0	25	12	US-11-121-849-208795
c 43	13.4	67.0	25	12	US-11-121-849-257563
c 44	13.4	67.0	25	12	US-11-121-849-285022
c 45	13.4	67.0	25	12	US-11-121-849-322158

ALIGNMENTS

RESULT 1

US-11-121-849-529681

; Sequence 529681, Application US/11121849

; Publication No. US20050272080A1

; GENERAL INFORMATION:

; APPLICANT: John Palma

; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded

; FILE REFERENCE: 3684.1

; CURRENT APPLICATION NUMBER: US/11/121,849

; CURRENT FILING DATE: 2005-05-03

; PRIOR APPLICATION NUMBER: 60/567,949

; PRIOR FILING DATE: 2004-05-03

; NUMBER OF SEQ ID NOS: 673904

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 529681

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapien

; US-11-121-849-529681

Query Match 82.0%; Score 16.4; DB 12; Length 25;
Best Local Similarity 94.4%; Pred No. 1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTTTCACCAATGGAAG 19

|||||

Db 1 CTTTCACCAATGGAAG 18

RESULT 2

US-11-121-849-447577/c

; Sequence 447577, Application US/11121849

; Publication No. US20050272080A1

; GENERAL INFORMATION:

; APPLICANT: John Palma

; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded

; FILE REFERENCE: 3684.1

; CURRENT APPLICATION NUMBER: US/11/121,849

; CURRENT FILING DATE: 2005-05-03

; PRIOR APPLICATION NUMBER: 60/567,949

; PRIOR FILING DATE: 2004-05-03

; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 447577
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-447577

Query Match 76.0%; Score 15.2; DB 12; Length 25;
Best Local Similarity 85.0%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCTTCCACCAAAATGGAAC 20
|||||
DB 20 GCTTCCACCTAGTTGAACC 1

RESULT 3

US-11-136-527-278180
; Sequence 278180, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Mounts, William M
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 278180
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-278180

Query Match 76.0%; Score 15.2; DB 12; Length 25;
Best Local Similarity 85.0%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCTTCCACCAAAATGGAAC 20
|||||
DB 3 GCTTCCAGCTAATGGAATC 22

RESULT 4

US-11-121-849-634116/c
; Sequence 634116, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 634116
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-634116

Query Match 75.0%; Score 15; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTCCACCAAAATGGA 17
|||||
DB 15 TTTCCACCAAAATGGA 1

RESULT 5

US-11-121-849-583444
; Sequence 583444, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 583444
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-583444

Query Match 74.0%; Score 14.8; DB 12; Length 25;
Best Local Similarity 88.9%; Pred. No. 6.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TTTCCACCAAAATGGAAC 20
|||||
DB 6 TTCCACCAAACTGGAAC 23

RESULT 6

US-10-310-914A-323453
; Sequence 323453, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CFUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 323453
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-323453

Query Match 72.0%; Score 14.4; DB 8; Length 24;
Best Local Similarity 62.5%; Pred. No. 9.7e+02;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTTCCACCAAAATG 16
|||||
DB 4 GCUUCCACCAUAUGG 19

RESULT 7

US-11-121-849-206297/c
; Sequence 206297, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays

US-11-121-849-206856

US-11-121-849-191
; Sequence 191, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:

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/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 191
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-191

Query Match      71.0%; Score 14.2; DB 12; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CTTTCACCAAAATGGGAAGC 20
        |||||
Db       4 CATGCACCTAATGGGAAGC 22

RESULT 13
US-11-121-849-345854
/ Sequence 345854, Application US/11/121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 345854
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-345854

Query Match      71.0%; Score 14.2; DB 12; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CTTTCACCAAAATGGGAAGC 20
        |||||
Db       4 CATGCACCTAATGGGAAGC 22

RESULT 14
US-11-121-849-673774
/ Sequence 673774, Application US/11/121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 673774
/ LENGTH: 25
/ TYPE: DNA
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/ ORGANISM: Homo sapien
US-11-121-849-673774

Query Match      71.0%; Score 14.2; DB 12; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CTTTCACCAAAATGGGAAGC 20
        |||||
Db       4 CATGCACCTAATGGGAAGC 22

RESULT 15
US-11-121-849-673775
/ Sequence 673775, Application US/11/121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 673775
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-673775

Query Match      71.0%; Score 14.2; DB 12; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CTTTCACCAAAATGGGAAGC 20
        |||||
Db       3 CATGCACCTAATGGGAAGC 21

Search completed: March 4, 2006, 03:54:50
Job time : 497.289 secs
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 4, 2006, 01:49:48 ; Search time 417.368 Seconds
(without alignments)
396.263 Million cell updates/sec

Title: US-09-701-583A-14

Perfect score: 20

Sequence: 1 gcttcacaaattggaagc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 10900902

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:

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- 2: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq*
- 3: /cgn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq*
- 4: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq*
- 5: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq*
- 6: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq*
- 7: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq*
- 8: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq*
- 9: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq*
- 10: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	6	US-10-220-033-5
2	20	100.0	20	9	US-10-984-919-532
3	18	90.0	18	9	US-10-984-919-1273
4	18	90.0	20	6	US-10-189-267-36
5	18	90.0	20	6	US-10-189-267-182
6	16	80.0	16	9	US-10-984-919-1275
7	16	80.0	18	5	US-10-146-058-79
8	16	80.0	18	9	US-10-984-919-1215
9	15.8	79.0	25	10	US-11-036-317-862259
10	15.8	79.0	25	10	US-11-036-317-873649
11	15.8	79.0	25	10	US-11-036-317-940468
12	15.2	76.0	25	7	US-10-719-956-259831
13	15	75.0	15	9	US-10-984-919-1274
14	14.8	74.0	25	10	US-11-060-756-239401
15	14.4	72.0	25	8	US-10-719-900-974400
16	14.4	72.0	25	9	US-10-956-157-147123
17	14.4	72.0	25	10	US-11-036-317-915488
18	14.4	72.0	25	10	US-11-036-317-986433
19	14.2	71.0	20	3	US-09-922-549B-60
20	14.2	71.0	20	6	US-10-114-739A-60
21	14.2	71.0	25	7	US-10-681-773-64719
22	14.2	71.0	25	7	US-10-681-773-103539
23	14.2	71.0	25	7	US-10-719-956-585916

C 24	14.2	71.0	25	8	US-10-719-900-930639	Sequence 930639,
C 25	14.2	71.0	25	9	US-10-809-189-6827	Sequence 6827, Ap
C 26	14.2	71.0	25	10	US-11-036-317-862258	Sequence 862258,
C 27	14.2	71.0	25	10	US-11-036-317-873648	Sequence 873648,
C 28	14.2	71.0	25	10	US-11-036-317-940467	Sequence 940467,
C 29	14.2	71.0	25	10	US-11-060-756-63888	Sequence 63888, A
C 30	14.2	71.0	25	10	US-11-060-756-63903	Sequence 63903, A
C 31	14.2	71.0	25	10	US-11-060-756-260911	Sequence 260911,
C 32	14.2	71.0	25	10	US-11-060-756-262958	Sequence 262958,
C 33	14.2	71.0	25	10	US-11-060-756-277348	Sequence 277348,
C 34	14	70.0	25	7	US-10-719-956-313402	Sequence 313402,
C 35	13.8	69.0	17	3	US-09-776-474-972	Sequence 972, App
C 36	13.8	69.0	19	9	US-10-898-660-73	Sequence 73, Appl
C 37	13.8	69.0	19	9	US-10-898-660-185	Sequence 185, App
C 38	13.8	69.0	25	7	US-10-719-956-121933	Sequence 121933,
C 39	13.8	69.0	25	7	US-10-719-956-612371	Sequence 612371,
C 40	13.8	69.0	25	7	US-10-719-956-623123	Sequence 623123,
C 41	13.8	69.0	25	8	US-10-719-900-379911	Sequence 379911,
C 42	13.8	69.0	25	8	US-10-719-900-415013	Sequence 415013,
C 43	13.8	69.0	25	8	US-10-719-900-492824	Sequence 492824,
C 44	13.8	69.0	25	9	US-10-956-157-131171	Sequence 131171,
C 45	13.8	69.0	25	10	US-11-036-317-789786	Sequence 789786,

ALIGNMENTS

RESULT 1
US-10-220-033-5
; Sequence 5, Application US/10220033
; Publication No. US20030186906A1
; GENERAL INFORMATION:
; APPLICANT: Schlingsienstepen, Karl-Hermann
; TITLE OF INVENTION: Mixture comprising an inhibitor or suppressor of a gene
; TITLE OF INVENTION: and a molecule binding to an expression product of that gene
; FILE REFERENCE: P68119US0
; CURRENT APPLICATION NUMBER: US/10/220,033
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: PCT/EP01/02694
; PRIOR FILING DATE: 2001-03-10
; PRIOR APPLICATION NUMBER: EP00105190.3
; PRIOR FILING DATE: 2000-03-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
; OTHER INFORMATION: oligonucleotide
US-10-220-033-5
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTTTCACCAAAATTCGAAGC 20
DB 1 GCTTTCACCAAAATTCGAAGC 20
RESULT 2
US-10-984-919-532
; Sequence 532, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlingsienstepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763US0

; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 532
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-532

Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCCACCAAAATTGGAAGC 20
|||||
Db 1 GCTTCCACCAAAATTGGAAGC 20

RESULT 3
US-10-984-919-1273
; Sequence 1273, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1273
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-1273

Query Match 90.0%; Score 18; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTTCCACCAAAATTGGAAG 19
|||||
Db 1 CTTTCCACCAAAATTGGAAG 18

RESULT 4
US-10-189-267-36
; Sequence 36, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie

; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-36

Query Match 90.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCCACCAAAATTGGA 18
|||||
Db 3 GCTTCCACCAAAATTGGA 20

RESULT 5
US-10-189-267-182/c
; Sequence 182, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 182
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-182

Query Match 90.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCCACCAAAATTGGA 18
|||||
Db 18 GCTTCCACCAAAATTGGA 1

RESULT 6
US-10-984-919-1275
; Sequence 1275, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1275
; LENGTH: 16
; TYPE: DNA


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RESULT 10
US-11-036-317-873649/c
; Sequence 873649, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 873649
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-873649

Query Match          79.0%; Score 15.8; DB 10; Length 25;
Best Local Similarity 89.5%; Pred. No. 5.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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US-11-036-317-940468/c
; Sequence 940468, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
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; LENGTH: 25
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US-11-036-317-940468

Query Match          79.0%; Score 15.8; DB 10; Length 25;
Best Local Similarity 89.5%; Pred. No. 5.7e+02;
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RESULT 12
US-10-719-956-259831/c
; Sequence 259831, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
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; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 259831
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; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-259831

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Best Local Similarity 85.0%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db      23  GCTGTACGAAATTTGAAGC 4

RESULT 13
US-10-984-919-1274
; Sequence 1274, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1274
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-1274

Query Match          75.0%; Score 15; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6  CACCAAAATTTGGAAGC 20
Db      1  CACCAAAATTTGGAAGC 15

RESULT 14
US-11-060-756-239401
; Sequence 239401, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
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; SEQ ID NO 239401
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-239401
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Best Local Similarity 88.9%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTTTCACCAAAATTGGAAG 19
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DB 3 CTTTCACCAAAATTGAGG 20
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RESULT 15
US-10-719-900-974400/c
; Sequence 974400, Application US/10719900
; Publication No. US200500261641
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 974400
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-974400

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Best Local Similarity 93.8%; Pred. No. 3e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 19 TCACCAAAAGTGAAGC 4
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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SUMMARIES

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1	18	100.0	18	6 A40535	A40535 Sequence 72
2	18	100.0	18	6 A89061	A89061 Sequence 12
3	18	100.0	18	6 BD065894	BD065894 An antisense
4	18	100.0	18	6 BD234905	BD234905 A method
5	18	100.0	18	6 CS123678	CS123678 Sequence
6	18	100.0	18	6 AR232815	AR232815 Sequence
7	18	100.0	18	6 AX008976	AX008976 Sequence
8	18	100.0	18	6 AX030110	AX030110 Sequence
9	18	100.0	18	6 AX252494	AX252494 Sequence
10	18	100.0	18	6 AX316431	AX316431 Sequence
11	18	100.0	22	6 BD234967	BD234967 A method
12	18	100.0	22	6 AX009038	AX009038 Sequence
13	18	100.0	27	6 AX113805	AX113805 Sequence
14	16	88.9	16	6 A89129	A89129 Sequence 12
15	16	88.9	16	6 BD066642	BD066642 An antisense
16	16	88.9	16	6 BD234928	BD234928 A method
17	16	88.9	16	6 AX008999	AX008999 Sequence
18	16	88.9	20	6 A88381	A88381 Sequence 52

19	16	88.9	20	6 A90348	A90348 Sequence 52
20	16	88.9	20	6 BD065894	BD065894 An antisense
21	16	88.9	20	6 BD234904	BD234904 A method
22	16	88.9	20	6 BD234965	BD234965 A method
23	16	88.9	20	6 CS123678	CS123678 Sequence
24	16	88.9	20	6 AX008975	AX008975 Sequence
25	16	88.9	20	6 AX009036	AX009036 Sequence
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27	14	77.8	17	6 BD203422	BD203422 Method an
28	13.8	76.7	20	6 AR130778	AR130778 Sequence
c 29	13.4	74.4	30	6 CS130581	CS130581 Sequence
c 30	13	72.2	17	6 BD203423	BD203423 Method an
c 31	12.8	71.1	22	6 AR393715	AR393715 Sequence
32	12.4	68.9	20	6 AR647382	AR647382 Sequence
33	12.4	68.9	20	6 AR654435	AR654435 Sequence
c 34	12.4	68.9	24	6 AR321595	AR321595 Sequence
35	12.4	68.9	38	6 A35024	A35024 Synthetic P
c 36	12.2	67.8	18	6 AR299597	AR299597 Sequence
c 37	12.2	67.8	23	6 BD184058	BD184058 Method an
c 38	12.2	67.8	23	6 AX742234	AX742234 Sequence
c 39	12.2	67.8	23	6 AX798838	AX798838 Sequence
40	12.2	67.8	24	6 AR075414	AR075414 Sequence
c 41	12.2	67.8	24	6 BD176117	BD176117 Anticoagu
42	12.2	67.8	25	6 CO986684	CO986684 Sequence
43	12.2	67.8	25	6 AR455613	AR455613 Sequence
44	12.2	67.8	25	6 AX353402	AX353402 Sequence
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ALIGNMENTS

RESULT 1
A40535
LOCUS A40535 18 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 72 from Patent WO9425578.
ACCESSION A40535
VERSION A40535.1 GI:2296570
KEYWORDS
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS
TITLE
JOURNAL
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ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
Patent: WO 9425578-A 72 10-NOV-1994;
BIOGNOSTIK GES (DE)

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGCATGCTATTGTGA 18
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DB 1 CGGCATGCTATTGTGA 18

RESULT 2
A89061
LOCUS A89061 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1209 from Patent WO9833904.
ACCESSION A89061
VERSION A89061.1 GI:6737631
KEYWORDS
SOURCE unidentified
ORGANISM unclassified

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unclassified sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 983904-A 1209 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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RESULT 3
BD066574 18 bp DNA linear PAT 27-AUG-2002
LOCUS An antisense oligonucleotide preparation method.
DEFINITION BD066574
ACCESSION BD066574
VERSION JP 2001511000-A/1209.
KEYWORDS unclassified.
SOURCE unclassified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1209 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/1209
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
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BD234905 18 bp DNA linear PAT 17-JUL-2003
LOCUS A method for stimulating the immune system.
DEFINITION BD234905
ACCESSION BD234905
VERSION BD234905.1 GI:33044675
KEYWORDS JP 2002517434-A/9.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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RESULT 5
CS123679 18 bp DNA linear PAT 16-JUL-2005
LOCUS Sequence 30 from Patent WO2005059133.
DEFINITION CS123679
ACCESSION CS123679
VERSION CS123679.1 GI:70912172
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Schlingensiepen,K.H.
TITLE Combination therapy associating a tgf-beta antagonist with a
chemotherapeutic agent
JOURNAL Patent: WO 2005059133-A 30 30-JUN-2005;
Antisense Pharma GmbH (DE)
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LOCUS Sequence 30 from Patent WO2005059133.
DEFINITION CS123679
ACCESSION CS123679
VERSION CS123679.1 GI:70912172
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Schlingensiepen,K.H.
TITLE Combination therapy associating a tgf-beta antagonist with a
chemotherapeutic agent
JOURNAL Patent: WO 2005059133-A 30 30-JUN-2005;
Antisense Pharma GmbH (DE)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
TITLE A method for stimulating the immune system
JOURNAL Patent: JP 2002517434-A 9 18-JUN-2002;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Homo sapiens (human)
PN JP 2002517434-A/9
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN,REINAR SCHLINGENSIEPEN,WOLFGANG PI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
PC 00,A61P35/00,
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AR232815 LOCUS 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 72 from patent US 6455689.
ACCESSION AR232815
VERSION AR232815.1 GI:27275153
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
(TGF-.beta.)
JOURNAL Patent: US 6455689-A 72 24-SEP-2002;
Biognostik Gesellschaft fur Biomolekulare Diagnostik mbH;
Gottingen;
EPX; Location/Qualifiers
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Db 1 CGGCATGCTATTTTGTA 18
RESULT 7
LOCUS AX008976 18 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 9 from Patent WO9963975.
ACCESSION AX008976
VERSION AX008976.1 GI:9996350
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE A method for stimulating the immune system
JOURNAL Patent: WO 9963975-A 9 16-DEC-1999;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
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Db 1 CGGCATGCTATTTTGTA 18
RESULT 8
LOCUS AX030110 18 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 72 from Patent EP1008649.
ACCESSION AX030110
VERSION AX030110.1 GI:10190327

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2 (tgf-b2)
JOURNAL Patent: EP 1008649-A 72 14-JUN-2000;
BIOGNOSTIK GES (DE)
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Db 1 CGGCATGCTATTTTGTA 18
RESULT 9
LOCUS AX252494 18 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 4 from Patent WO0168146.
ACCESSION AX252494
VERSION AX252494.1 GI:15985765
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE Mixture comprising an inhibitor or suppressor of a gene and a
molecule binding to an expression product of that gene
JOURNAL Patent: WO 0168146-A 4 20-SEP-2001;
Biognostik Gesellschaft fuer biomolekulare Diagnostik mbH (DE)
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DEFINITION Sequence 72 from Patent EP1160319.
ACCESSION AX316431
VERSION AX316431.1 GI:17899604
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified sequences.

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REFERENCE
1
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 72 05-DEC-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
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Db 1 CGGCATGCTCTATTGTGA 18
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RESULT 11
BD234967 22 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION A method for stimulating the immune system.
ACCESSION BD234967
VERSION BD234967.1 GI:33044737
KEYWORDS JP 2002517434-A/71.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 22)
Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
A method for stimulating the immune system
Patent: JP 2002517434-A 71 18-JUN-2002;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
OS Homo sapiens (human)
PN JP 2002517434-A/71
PD 18-JUN-2002
PP 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG RI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
PC 00,A61P35/00
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
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RESULT 12
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LOCUS
DEFINITION A method for stimulating the immune system.
ACCESSION BD234967
VERSION BD234967.1 GI:33044737
KEYWORDS JP 2002517434-A/71.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 22)
Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
A method for stimulating the immune system
Patent: JP 2002517434-A 71 18-JUN-2002;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
OS Homo sapiens (human)
PN JP 2002517434-A/71
PD 18-JUN-2002
PP 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG RI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
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AX113805 27 bp DNA linear PAT 01-MAY-2001
LOCUS
DEFINITION Sequence 51 from Patent WO0127256.
ACCESSION AX113805
VERSION AX113805.1 GI:13939971
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
1
REFERENCE Wu,L., Carey,M.P. and Belldegrun,A.S.
AUTHORS Chimeric transcriptional regulatory element and methods for
TITLE prostate-targeted gene expression
JOURNAL Patent: WO 0127256-A 51 19-APR-2001;
The Regents of the University of California System (US)
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RESULT 14
AX89129 16 bp DNA linear PAT 23-JAN-2000
LOCUS
DEFINITION Sequence 1277 from Patent WO9833904.
ACCESSION AX89129
VERSION AX89129.1 GI:6737699
KEYWORDS unidentified
SOURCE
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LOCUS
AX009038 22 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 71 from Patent WO9963975.
ACCESSION AX009038
VERSION AX009038.1 GI:9996412
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1
REFERENCE Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
AUTHORS A method for stimulating the immune system
TITLE A method for stimulating the immune system
JOURNAL Patent: WO 9963975-A 71 16-DEC-1999;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
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Db 5 CGGCATGCTCTATTGTGA 22
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RESULT 13
AX113805 27 bp DNA linear PAT 01-MAY-2001
LOCUS
DEFINITION Sequence 51 from Patent WO0127256.
ACCESSION AX113805
VERSION AX113805.1 GI:13939971
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
1
REFERENCE Wu,L., Carey,M.P. and Belldegrun,A.S.
AUTHORS Chimeric transcriptional regulatory element and methods for
TITLE prostate-targeted gene expression
JOURNAL Patent: WO 0127256-A 51 19-APR-2001;
The Regents of the University of California System (US)
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Db 3 CGGCATGCTCTATTGTGA 20
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RESULT 14
AX89129 16 bp DNA linear PAT 23-JAN-2000
LOCUS
DEFINITION Sequence 1277 from Patent WO9833904.
ACCESSION AX89129
VERSION AX89129.1 GI:6737699
KEYWORDS unidentified
SOURCE
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ORGANISM      unidentified
unclassified sequences.
REFERENCE      1 (bases 1 to 16)
AUTHORS        Brysch, W. and Schlingensiepen, K.
TITLE          AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL        Patent: WO 9833904-A 1277 06-AUG-1998;
                BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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DEFINITION    An antisense oligonucleotide preparation method.
ACCESSION     BD066642
VERSION       BD066642.1 GI:22612245
KEYWORDS      JP 2001511000-A/1277.
SOURCE        unidentified
ORGANISM      unidentified
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REFERENCE      1 (bases 1 to 16)
AUTHORS        Schlingensiepen, K.H. and Brysch, W.
TITLE          An antisense oligonucleotide preparation method
JOURNAL        Patent: JP 2001511000-A 1277 07-AUG-2001;
                BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT        OS Unknown
                PN JP 2001511000-A/1277
                PD 07-AUG-2001
                PF 30-JAN-1998 JP 1998532533
                PR 31-JAN-1997 EP 97101531.8
                PI KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
                PC C12N15/11, C07H21/04, A61K31/70
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Title: US-09-701-583A-9

Perfect score: 18
Sequence: 1 cgcgcgtctctcttgc 18

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SUMMARIES

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1	18	100.0	18	US-08-535-249-72	Sequence 72, Appl
2	13.8	76.7	20	US-09-429-322-29	Sequence 29, Appl
3	13.4	74.4	20	US-10-053-662A-7	Sequence 7, Appl
4	13.2	73.3	25	US-09-396-196G-19083	Sequence 19083, A
5	13.2	73.3	25	US-09-396-196G-72258	Sequence 72258, A
6	12.8	71.1	22	US-09-526-193A-254	Sequence 254, App
7	12.4	68.9	20	US-10-393-905-35	Sequence 35, Appl
8	12.4	68.9	20	US-10-660-253-21	Sequence 21, Appl
9	12.4	68.9	24	US-09-460-555-3	Sequence 3, Appl
10	12.2	67.8	24	US-09-422-978-11332	Sequence 11332, A
11	12.2	67.8	24	US-08-273-402B-9	Sequence 11, Appl
12	12.2	67.8	25	US-09-903-013-11	Sequence 11, Appl
13	12.2	67.8	31	US-08-823-516-113	Sequence 113, App
14	12.2	67.8	31	US-08-759-038-134	Sequence 134, App
15	12.2	67.8	31	US-08-758-314-134	Sequence 134, App
16	12.2	67.8	31	US-09-684-938-134	Sequence 134, App
17	12.2	67.8	31	US-09-308-825A-134	Sequence 134, App
18	12.2	67.8	31	US-09-940-244-113	Sequence 113, App
19	12.2	67.8	31	US-09-381-212-113	Sequence 113, App
20	12.2	67.8	31	US-09-713-601A-113	Sequence 113, App
21	12	66.7	27	US-09-964-948-3	Sequence 3, Appl
22	11.8	66.7	30	US-08-479-487-65	Sequence 65, Appl
23	11.8	65.6	15	US-08-311-486C-105	Sequence 105, App
24	11.8	65.6	2	US-08-311-486C-631	Sequence 631, App

25	11.8	65.6	15	9	5182195-62	Patent No. 5182195
26	11.8	65.6	19	3	US-09-475-947A-61	Sequence 61, Appl
27	11.8	65.6	20	2	US-08-599-252-2	Sequence 2, Appl
28	11.8	65.6	20	2	US-08-436-074-2	Sequence 2, Appl
29	11.8	65.6	20	3	US-02-166-186-88	Sequence 88, Appl
30	11.8	65.6	20	3	US-09-166-186-132	Sequence 132, App
31	11.8	65.6	20	3	US-09-313-932-88	Sequence 88, Appl
32	11.8	65.6	20	3	US-09-313-932-132	Sequence 132, App
33	11.8	65.6	20	3	US-09-313-932-453	Sequence 453, Appl
34	11.8	65.6	20	3	US-09-887-145-43	Sequence 43, Appl
35	11.8	65.6	20	6	PCT-US96-06352-2	Sequence 2, Appl
36	11.8	65.6	20	6	PCT-US96-06583-2	Sequence 2, Appl
37	11.8	65.6	21	3	US-09-422-978-10510	Sequence 10510, A
38	11.8	65.6	21	3	US-09-382-552-124	Sequence 124, App
39	11.8	65.6	22	2	US-08-217-529-6	Sequence 6, Appl
40	11.8	65.6	22	6	PCT-US93-02259-13	Sequence 13, Appl
41	11.8	65.6	25	3	US-09-396-196G-118255	Sequence 118255, Sequence 118256
42	11.8	65.6	25	3	US-09-396-196G-118256	Sequence 118256, Sequence 118257
43	11.8	65.6	25	3	US-09-396-196G-118257	Sequence 118257, Sequence 118258
44	11.8	65.6	26	3	US-09-077-734-40	Sequence 40, Appl
45	11.8	65.6	30	3	US-09-276-147B-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-535-249-72
Sequence 72, Application US/08535249
Patent No. 6455689
GENERAL INFORMATION:
APPLICANT: Schlingensiepen, Georg-Ferdinand
APPLICANT: Brysch, Wolfgang
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Bogdahn, Ulrich
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
TITLE OF INVENTION: Immuno-suppressive effect of transforming-growth-factor beta
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESSES:
ADDRESS: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,249
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 849.7
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDBA UR
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown

TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-535-249-72

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Best Local Similarity 100.0%; Pred. No. 7.3;
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DB 1 CGGCATGCTATTGTA 18

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US-09-429-322-29
Sequence 29, Application US/09429322A
Patent No. 6190869
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Coweert
TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN KINASE C-THETA
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTS-0100
CURRENT APPLICATION NUMBER: US/09/429,322A
CURRENT FILING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 29
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-429-322-29

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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 2 GGCATGCTATTGTA 18

RESULT 3
US-10-053-662A-7
Sequence 7, Application US/10053662A
Patent No. 6916618
GENERAL INFORMATION:
APPLICANT: Alexandra Charlesworth
APPLICANT: Falvia Spilito
APPLICANT: Guerrino Meneguzzi
APPLICANT: John Baird
APPLICANT: Ketch Linder
TITLE OF INVENTION: ISOLATION OF THE LAMININ Y2 GENE IN
TITLE OF INVENTION: HORSES AND ITS USE IN DIAGNOSING JUNCTIONAL EPIDERMOLYSIS
FILE REFERENCE: P84us4
CURRENT APPLICATION NUMBER: US/10/053,662A
CURRENT FILING DATE: 2002-01-24
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: primer
US-10-053-662A-7

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Best Local Similarity 93.3%; Pred. No. 1.6e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CATGCTATTGTA 18
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DB 1 CCTGCTATTGTA 15

RESULT 4
US-09-396-196G-19083
Sequence 19083, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19083
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-19083

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RESULT 5
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Sequence 72258, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
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LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
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QY 1 CGGCATGCTATTGTA 18
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RESULT 6
US-09-526-193A-254/c
Sequence 254, Application US/09526193A


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; Patent No. 6617122
; GENERAL INFORMATION:
; APPLICANT: Hayden, Michael R.
; APPLICANT: Brooks-Wilson, Angela R.
; APPLICANT: Pimstone, Simon N.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING
; FILE OF INVENTION: CHOLESTEROL LEVELS
; FILE REFERENCE: 50110/002005
; CURRENT APPLICATION NUMBER: US/09/526,193A
; CURRENT FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/124,702
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 60/138,048
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/139,600
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/151,977
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 287
; SOFTWARE: FastSeq for Windows Version 4.0
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; US-09-526-193A-254

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Best Local Similarity 87.5%; Pred. No. 3.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB      21 GCATTTCTATTTTGA 6

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; Sequence 35, Application US/10393905
; GENERAL INFORMATION:
; APPLICANT: OETTER, PETER
; APPLICANT: LIBERMANN, TOMIA
; APPLICANT: GOLDRING, MARY
; TITLE OF INVENTION: USE OF TRANSCRIPTION FACTORS FOR TREATING INFLAMMATION
; FILE REFERENCE: 49923CIP (72037)
; CURRENT APPLICATION NUMBER: US/10/393,905
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: PCT/US01/29340
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/234,379
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-10-393-905-35

Query Match      68.9%; Score 12.4; DB 3; Length 20;
Best Local Similarity 92.9%; Pred. No. 5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 CATGCTATTTTGT 17
DB      2 CATGCTTTTGT 15

RESULT 8
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US-10-660-253-21
; Sequence 21, Application US/10660253
; Patent No. 6889143
; GENERAL INFORMATION:
; APPLICANT: Benlike, Mark A.
; APPLICANT: Lingyan, Huang
; APPLICANT: Owczarzy, Richard
; APPLICANT: Walder, Joseph A.
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR ESTIMATING THE MELTING TEMPERATURE (Tm) F
; FILE REFERENCE: 03988/100K297-US1
; CURRENT APPLICATION NUMBER: US/10/660,253
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 60/410,663
; PRIOR FILING DATE: 2002-09-12
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
; US-10-660-253-21

Query Match      68.9%; Score 12.4; DB 3; Length 20;
Best Local Similarity 92.9%; Pred. No. 5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 ATGCTATTTTGA 18
DB      2 ATGTATATTTTGA 15

RESULT 9
US-09-460-555-3/c
; Sequence 3, Application US/09460555
; Patent No. 6563014
; GENERAL INFORMATION:
; APPLICANT: Albert Einstein College of Medicine of Yeshiva University
; APPLICANT: Goldstein, Harris
; APPLICANT: Paul, Jessie B.
; TITLE OF INVENTION: SELF-CONTAINED SYSTEM FOR SUSTAINED VIRAL REPLICATION
; FILE REFERENCE: 96700/552
; CURRENT APPLICATION NUMBER: US/09/460,555
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 24
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: primer
; US-09-460-555-3

Query Match      68.9%; Score 12.4; DB 3; Length 24;
Best Local Similarity 92.9%; Pred. No. 5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 ATGCTATTTTGA 18
DB      20 ATGCTATTTTGA 7

RESULT 10
US-09-422-978-11332/c
; Sequence 11332, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
```

TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CPI
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/238,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO: 11332
LENGTH: 18
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: primer_bind
LOCATION: 1..18
OTHER INFORMATION: downstream amplification primer 99-4284 for SEQ 3467, in compleme
US-09-422-978-11332

Query Match 67.8%; Score 12.2; DB 3; Length 18;
Best Local Similarity 82.4%; Pred. No. 6.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGCACTCTATTGTGA 18
DB 18 GGCACTCTACTTTGCA 2

RESULT 11
US-08-273-402B-9
Sequence 9, Application US/08273402B
Patent No. 5958403
GENERAL INFORMATION:
APPLICANT: Strom, Terry
APPLICANT: Rubin-Kelly, Vicki E.
APPLICANT: Liberman, Towia
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR
TITLE OF INVENTION: PREVENTION OF GRAFT REJECTION
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,402B
FILING DATE: 11-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/024,569
FILING DATE: 01-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/843,731
FILING DATE: 28-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark, Esq.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 05311/012001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:

LENGTH: 24
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-273-402B-9

Query Match 67.8%; Score 12.2; DB 2; Length 24;
Best Local Similarity 82.4%; Pred. No. 6.3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGCACTCTATTGTGA 18
DB 1 GGCACTCTACTTTGGA 17

RESULT 12
US-09-903-013-11
Sequence 11, Application US/09903013
Patent No. 6685950
GENERAL INFORMATION:
APPLICANT: Weber, Olaf
APPLICANT: Schlapp, Tobias
APPLICANT: Siegling, Angela
APPLICANT: Knorr, Andreas
APPLICANT: Hirth-Dietrich, Claudia
TITLE OF INVENTION: Use of Strains of Parapoxvirus Ovis for Producing Antiviral Medic
FILE REFERENCE:lea 34 376
CURRENT APPLICATION NUMBER: US/09/903,013
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: DE10033582.9
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: DE10122451.6
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.0
SEQ ID NO 11
LENGTH: 25
TYPE: DNA
ORGANISM: Mus sp.
US-09-903-013-11

Query Match 67.8%; Score 12.2; DB 3; Length 25;
Best Local Similarity 82.4%; Pred. No. 6.3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGCACTCTATTGTGA 18
DB 1 GGCACTCTACTTTGGA 17

RESULT 13
US-08-823-516-113/c
Sequence 113, Application US/08823516
Patent No. 5994069
GENERAL INFORMATION:
APPLICANT: Hall, Jeff G.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Mast, Andrea L.
APPLICANT: Brow, Mary Ann D.
TITLE OF INVENTION: Detection Of Nucleic Acids By Multiple
TITLE OF INVENTION: Sequential Invasive Cleavages
NUMBER OF SEQUENCES: 163
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,516
FILING DATE: 24-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/01072
FILING DATE: 21-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/759,038
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,314
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/756,386
FILING DATE: 29-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/682,853
FILING DATE: 12-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,491
FILING DATE: 24-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02736
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
FEATURE:
NAME/KEY: misc difference
LOCATION: replace(1..2, "")
OTHER INFORMATION: /note= "The residues at these
OTHER INFORMATION: positions are a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)."
FEATURE:
NAME/KEY: misc difference
LOCATION: replace(3, "")
OTHER INFORMATION: /note= "The residue at this
OTHER INFORMATION: position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)."
FEATURE:
NAME/KEY: misc difference
LOCATION: replace(4..5, "")
OTHER INFORMATION: /note= "The residues at these
OTHER INFORMATION: positions are a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate)."
FEATURE:
NAME/KEY: misc difference
LOCATION: replace(6..8, "")
OTHER INFORMATION: /note= "The residues at these
OTHER INFORMATION: positions are a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)."
FEATURE:
NAME/KEY: misc difference
LOCATION: replace(9, "")
OTHER INFORMATION: /note= "The residue at this
OTHER INFORMATION: position is a 2'deoxyguanosine 5'-O-(1-Thiomonophosphate)."
FEATURE:
NAME/KEY: misc difference
LOCATION: replace(10, "")
OTHER INFORMATION: /note= "The residue at this
OTHER INFORMATION: position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)."
US-08-823-516-113

Query Match 67.8%; Score 12.2; DB 2; Length 31;

Best Local Similarity 82.4%; Pred. No. 6.4e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
CY 2 GGCATGCTATTTGTA 18
DB 31 GGCCTGTTATTTGTA 15
RESULT 14
US-08-759-038-134/C
Sequence 134, Application US/08759038
Patent No. 6090543
GENERAL INFORMATION:
APPLICANT: Prudent, James R.
APPLICANT: Hall, Jeff G.
APPLICANT: Lyamchev, Victor I.
APPLICANT: Brow, Mary Ann D.
APPLICANT: Dahlberg, James E.
TITLE OF INVENTION: Cleavage Of Nucleic Acids
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,038
FILING DATE: 02-DEC-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 29-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/682,853
FILING DATE: 12-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,491
FILING DATE: 24-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02574
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
FEATURE:
NAME/KEY: misc difference
LOCATION: replace(1..2, "")
OTHER INFORMATION: /note= "The residues at these
OTHER INFORMATION: positions are a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)."
FEATURE:
NAME/KEY: misc difference
LOCATION: replace(3, "")
OTHER INFORMATION: /note= "The residue at this
OTHER INFORMATION: position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)."
FEATURE:
NAME/KEY: misc difference
LOCATION: replace(4..5, "")

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OTHER INFORMATION: /note="The residues at these
OTHER INFORMATION: positions are a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate).
FEATURE:
NAME/KEY: misc_difference
LOCATION: replace(6..8, "")
OTHER INFORMATION: /note="The residues at these
OTHER INFORMATION: positions are a 2'deoxythymidine 5'-O-(1-Thiomonophosphate).
FEATURE:
NAME/KEY: misc_difference
LOCATION: replace(9, "")
OTHER INFORMATION: /note="The residue at this
OTHER INFORMATION: position is a 2'deoxyguanosine 5'-O-(1-Thiomonophosphate)."
FEATURE:
NAME/KEY: misc_difference
LOCATION: replace(10, "")
OTHER INFORMATION: /note="The residue at this
OTHER INFORMATION: position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)."
US-08-759-038-134

Query Match 67.8%; Score 12.2; DB 3; Length 31;
Best Local Similarity 82.4%; Pred. No. 6.4e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGCGATGCTATTGTGA 18
DB 31 GGCGTGTATTGTGA 15

RESULT 15
US-08-758-314-134/C
Sequence 134, Application US/08758314
Patent No. 6090606
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Improved Cleavage Agents
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,314
FILING DATE: 02-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 29-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/682,853
FILING DATE: 12-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,491
FILING DATE: 24-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02575
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
FEATURE:
NAME/KEY: misc_difference
LOCATION: replace(1..2, "")
OTHER INFORMATION: /note="The residues at these
OTHER INFORMATION: positions are a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)."
FEATURE:
NAME/KEY: misc_difference
LOCATION: replace(3, "")
OTHER INFORMATION: /note="The residue at this
OTHER INFORMATION: position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)."
FEATURE:
NAME/KEY: misc_difference
LOCATION: replace(4..5, "")
OTHER INFORMATION: /note="The residues at these
OTHER INFORMATION: positions are a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate)."
FEATURE:
NAME/KEY: misc_difference
LOCATION: replace(6..8, "")
OTHER INFORMATION: /note="The residues at these
OTHER INFORMATION: positions are a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)."
FEATURE:
NAME/KEY: misc_difference
LOCATION: replace(9, "")
OTHER INFORMATION: /note="The residue at this
OTHER INFORMATION: position is a 2'deoxyguanosine 5'-O-(1-Thiomonophosphate)."
FEATURE:
NAME/KEY: misc_difference
LOCATION: replace(10, "")
OTHER INFORMATION: /note="The residue at this
OTHER INFORMATION: position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)."
US-08-758-314-134

Query Match 67.8%; Score 12.2; DB 3; Length 31;
Best Local Similarity 82.4%; Pred. No. 6.4e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGCGATGCTATTGTGA 18
DB 31 GGCGTGTATTGTGA 15
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Search completed: March 4, 2006, 02:07:27
Job time : 70.1579 secs